



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 104996

TO: Phillip Gambel
Location: cm1/9e12
Art Unit: 1644
Friday, October 03, 2003

Case Serial Number: 09758173

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Gambel,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

RUSH

09 / 758173

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:10:05 ; Search time 76.372 Seconds
(without alignments)
8304.972 Million cell updates/sec

Title: US-09-758-173-7
Perfect score: 1437
Sequence: 1 ATGGGTGGAGCCCTCATCTT.....CCCTGTCTCCGGTAAATGA 1437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1437	100.0	1437	3	US-08-487-550-7 Sequence 7, Appli
2	1437	100.0	1437	4	US-09-526-098-7 Sequence 7, Appli
3	1177.8	82.0	19040	4	US-09-343-485A-3 Sequence 3, Appli
4	1155.8	80.4	1576	1	US-08-157-101A-6 Sequence 6, Appli
5	1142	79.5	1350	1	US-08-157-101A-9 Sequence 9, Appli
6	1131.8	78.8	1617	2	US-08-378-939-9 Sequence 9, Appli
7	1127.4	78.5	9209	1	US-08-149-099C-3 Sequence 3, Appli
8	1127.4	78.5	9209	1	US-08-476-275-2 Sequence 2, Appli
9	1127.4	78.5	9209	4	US-08-478-967A-3 Sequence 3, Appli
10	1127.4	78.5	9209	4	US-08-475-815B-3 Sequence 3, Appli
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13	1127.4	78.5	18986	4	US-09-343-485A-2 Sequence 2, Appli
14	1120.6	78.0	8120	3	US-09-027-449-68 Sequence 68, Appli
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22	1118.2	77.8	1428	2	US-08-635-878-19 Sequence 19, Appli
23	1118.2	77.8	1428	3	US-08-770-057-19 Sequence 19, Appli
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Query Match

100.0% ; Score 1437 ; DB 3 ; Length 1437 ;

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40 1108 77.1 1418 4 US-08-793-450-7 Sequence 3, Appli
41 1102 76.7 6557 1 US-08-286-740-3 Sequence 3, Appli
42 1102 76.7 6557 5 PCT-US95-09576-3 Sequence 3, Appli
43 1087 75.6 1567 3 US-09-049-672A-17 Sequence 17, Appli
44 1079 75.1 1655 3 US-09-049-672A-21 Sequence 21, Appli
45 1036.6 72.1 1329 5 PCT-US96-13152-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-487-550-7
; Sequence 7, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1437
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1437
US-08-487-550-7

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 19:53:01 ; Search time 284.274 Seconds
(without alignments)
12894.584 Million cell updates/sec

Title: US-09-758-173-7
Perfect score: 1437
Sequence: 1 ATGGGTTGGAGCTCATCTT.....CCCTGTCCTCCGGTAATGA 1437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 3: /cgn2.6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 12: /cgn2.6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2.6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1216	84.6	1616	10	US-09-822-830A-572
7	1186	82.5	1798	9	US-09-925-299-230
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9	1185	82.5	1430	12	US-10-225-108A-1
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14	1165.4	81.1	1615	9	US-09-822-849A-111
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16	1158.4	80.6	6284	13	US-10-066-895-14
17					Sequence 14, Appl

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18	1142.8	79.5	1598	9	US-09-822-849A-103	Sequence 103, App
19	1142.8	79.5	1634	10	US-09-822-830A-303	Sequence 303, App
20	1141.4	79.4	1356	10	US-09-822-698A-27	Sequence 27, Appl
21	1141.4	79.4	1431	12	US-10-325-108A-15	Sequence 15, Appl
22	1138.6	79.2	1347	10	US-09-736-371B-20	Sequence 20, Appl
23	1138.6	79.2	1590	9	US-09-822-849A-114	Sequence 114, App
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25	1133.4	78.9	1599	10	US-09-954-456-789	Sequence 789, App
26	1133.4	78.9	1599	10	US-09-954-456-1604	Sequence 1604, App
27	1133.4	78.9	1599	12	US-09-873-319-445	Sequence 445, App
28	1133.4	78.9	1599	12	US-09-960-706-704	Sequence 704, App
29	1133.4	78.9	1599	12	US-09-873-367C-1010	Sequence 1010, Ap
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31	1130.2	78.6	1449	10	US-09-747-669-2	Sequence 2, Appli
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33	1130.2	78.6	1449	14	US-10-390-703-2	Sequence 2, Appli
34	1129.2	78.6	9182	11	US-09-927-122-41	Sequence 41, Appl
35	1129.2	78.6	9182	11	US-09-927-121B-89	Sequence 89, Appl
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37	1127.4	78.5	9209	10	US-09-911-703-3	Sequence 3, Appli
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41	1127.4	78.5	18986	13	US-10-109-853-2	Sequence 40, Appl
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45	1119	77.9	3300	14	US-10-020-786-2	

ALIGNMENTS

RESULT 1
US-09-948-429B-7
; Sequence 7, Application US/09948429B
; Patent No. US20020177689A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA USA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION NUMBER: US/09/348,429B

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021


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; INFORMATION FOR SEQ_ID NO: 7
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 1437 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: not relevant
;     TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..1437
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; FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 1..1437
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US-09-9498-429B-7

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DB	181	GGGAAGGGGCGGAATGGGTAGGTTTCATTAGAAAACAAACCGAAGCGTGGGACACACAGAA	240	
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DB	241	TACGCGCGTCTGTGAAGACAGATTACCATCTCCAGAGATGATTCCAAAAGCATCGCC	300	
QY	301	TATCTGCAAAATGAGCAGCCTGAAATCGAGGACACGCGCGTCTATTACTGTACTACATCC	360	
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DB	421	GGCGCCCTGGTCAACCGTCTCCTCAGCTAGCACCAAGGGGCCATCGGCTCTCCGCCCTGGCA	480	
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DB	481	CCCTCTCTCAGAGAGCACTCTGGGGGACACAGCGGCCCTGGGCTGCGCTGTCAGAGACTAC	540	
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QY	601	TTCCCGGGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCCTGGCCC	660	
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QY	901	GACCCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGCTGGAGGTGCATAATGCCAAGACA	960
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RESULT 2
US-10-124-807-7
Sequence 7, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
TITLE OF INVENTION: IMMUNOSUPPRESSANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 56.0907 Seconds
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1352.654 Million cell updates/sec

Title: US-09-758-173-8
Perfect score: 2561
Sequence: 1 MGWSLLFLVAVATRVQCE.....MHEALHNYTKSLSPGK 478

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:
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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2561	100.0	478	19	AAW63763 Macaque primatized
2	2561	100.0	478	23	AAU11644 Protein sequence o
3	2555	99.8	478	18	AAW01820 Primatized anti-hu
4	2205	86.1	468	24	ABP58275 Humanised 3D6 anti
5	2197	85.8	461	14	AA42162 Anti-HIV-1 recombi
6	2184.5	85.3	452	20	AAV29458 Recombinant immuno
7	2184.5	85.3	452	21	AAH30322 Humanised anti-IL-
8	2184.5	85.3	452	21	AAV7766 Humanised anti-IL-
9	2184.5	85.3	452	24	ABU59512 Humanised Mouse an

10	2184.5	85.3	452	24	ABU13799 Humanised mouse an
11	2183	85.2	474	23	AAO14065 Heavy chain protei
12	2183	85.2	474	24	ABU08017 Human monoclonal r
13	2180.5	85.1	449	23	AAO18400 Mature humanised m
14	2177.5	85.0	477	22	AAU14288 Human novel protei
15	2176	85.0	470	23	ABB81109 Anti-tissue factor
16	2176	85.0	470	24	ABP72748 Anti-tissue factor
17	2175.5	84.9	447	24	AAE33522 Human AQC2 heavy c
18	2175.5	84.9	452	19	AAW69316 Anti-IL-8 humanise
19	2172.5	84.8	475	13	AAK20057 Heavy chain of 3D6
20	2169.5	84.7	447	24	AAE33523 Human AQC2 heavy c
21	2169.5	84.7	461	22	AAU07745 Humanised monoclon
22	2165.5	84.6	447	24	AAE33524 Human AQC2 heavy c
23	2162	84.4	470	13	AAE22757 Reshaped CAMPATH-1
24	2161.5	84.4	444	21	AAE32283 Humanised anti-CD2
25	2160	84.3	449	24	ABF58273 Humanised 3D6 anti
26	2160	84.3	451	22	AAE12715 Human recombinant
27	2160	84.3	451	24	ABU58807 Mucin 1 (MUC-1) bi
28	2156.5	84.2	481	13	AAE24442 Sequence of antibo
29	2156	84.2	476	23	ABE81110 Anti-VEGF heavy ch
30	2154	84.1	449	21	AAV68810 A rat heavy chain
31	2151	84.0	477	15	AAE47453 ch184.12 H3 heavy
32	2149.5	83.9	731	22	AAW52156 Humanised HMF6-1 h
33	2149.5	83.9	741	22	AAW52159 Humanised HMF6-1 h
34	2148	83.9	470	23	AAE27923 Human C2B8 antibod
35	2148	83.9	470	24	ABE82832 Antibody C2B8 heav
36	2147	83.8	464	23	ABG91842 Human antibody fra
37	2147	83.8	464	23	ABG78151 Human Fv molecule
38	2144.5	83.7	729	22	AAW52158 Humanised HMF6-1 h
39	2144.5	83.7	739	22	AAW52151 Humanised HMF6-1 h
40	2140	83.6	582	22	AAH81987 Ganglioside Gb3 sp
41	2139	83.5	470	21	AAH08036 A dimeric anti-CD2
42	2138.5	83.5	459	14	AA42066 Human anti-HBs hea
43	2138.5	83.5	730	22	AAW52157 Humanised HMF6-1 h
44	2138.5	83.5	740	22	AAW52160 Humanised HMF6-1 h
45	2137.5	83.5	444	24	AAE34876 BIWA4/8 antibody h

ALIGNMENTS

RESULT 1	AAW63763	AAW63763 standard; Protein; 478 AA.
ID	AAW63763	standard; Protein; 478 AA.
AC	AAW63763	
DT	29-SEP-1998	(first entry)
DE	Macaque primatized 7B6 heavy chain protein.	
KW	Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;	
KW	CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;	
KW	T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;	
KW	immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;	
KW	T cell proliferation.	
OS	Macaque fascicularis.	
PN	WO9819706-A1.	
PD	14-MAY-1998.	
PF	29-OCT-1997; 97WO-US19906.	
PR	08-NOV-1996; 96US-0746361.	
PA	(IDEC-) IDEC PHARM CORP.	
PI	Anderson DR, Brams P, Hanna N;	
XX	WPI; 1998-286601/25.	
DR	N-PSDB; AAV35487.	

XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PS cells, e.g. graft rejection or tumours
XX
XX Example 7; Fig 4b; 87pp; English.
XX
CC This sequence represents a primatized form of the antibody 7B6 heavy
CC chain from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC MAB's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC MAB can be conjugated to a drug or toxin. MAB's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotypic reagents. MAB's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
XX Sequence 478 AA;

Query Match 100.0%; Score 2561; DB 19; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.2e-152;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLILFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMWFRQAP 60
DB 1 MGWSLILFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMWFRQAP 60
QY 61 GKGPWVGFI RNKPNGGTTEYAA SVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
DB 61 GKGPWVGFI RNKPNGGTTEYAA SVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
QY 121 YISHCRGVGYG YGFEFWGQALVTVSSASTKGPSVFLPAPSSKTSGGTAAALGCLVKDY 180
DB 121 YISHCRGVGYG YGFEFWGQALVTVSSASTKGPSVFLPAPSSKTSGGTAAALGCLVKDY 180
QY 181 FPEPTVSNVSGALTSVGHVTPPAVLQSSGLYSLSSVWVPSSSLGTQYICNVNHPKPSNT 240
DB 181 FPEPTVSNVSGALTSVGHVTPPAVLQSSGLYSLSSVWVPSSSLGTQYICNVNHPKPSNT 240
QY 241 KVDKKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE 300
DB 241 KVDKKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE 300
QY 301 DPEVKFNWYDGVGVHNAKTREEQYNSTYRVSVLTVLHODWLNKREYKCKVSNKALP 360
DB 301 DPEVKFNWYDGVGVHNAKTREEQYNSTYRVSVLTVLHODWLNKREYKCKVSNKALP 360
QY 361 APIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVAVESNGQPEN 420
DB 361 APIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVAVESNGQPEN 420
QY 421 NYKTTTPVLDSDGSFPLYSLKLVKDSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 478
DB 421 NYKTTTPVLDSDGSFPLYSLKLVKDSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 478

RESULT 2

AAU11644

ID AAU11644 standard; Protein; 478 AA.

XX

AC AAU11644;

XX

DT 12-MAR-2002 (first entry)

XX
DE
XX
KW Human; macaque monkey; light chain; primatised antibody; 7B6 antibody.
KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW graft-vs-host disease; immunosuppression; organ rejection;
KW interleukin-2; IL-2; mutant; mutein.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Macaca sp.
OS Synthetic.
PN WO200189567-A1.
XX
PD 29-NOV-2001.
XX
XX 22-MAY-2001; 2001WO-US16364.
PR
XX
XX 22-MAY-2000; 2000US-0576424.
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Hanna N, Brams P;
XX
XX WPI; 2002-089895/12.
DR N-PSDB; AAS17245.
XX
PT Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy -
XX
XX Example 8; Fig 4b; 89pp; English.
XX
CC The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus,
CC type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present protein
CC sequence represents the heavy chain of 7B6, a primatised antibody
CC used in the invention to induce apoptosis.
XX
XX Sequence 478 AA;

Query Match 100.0%; Score 2561; DB 23; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.2e-152;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLILFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMWFRQAP 60
DB 1 MGWSLILFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMWFRQAP 60
QY 61 GKGPWVGFI RNKPNGGTTEYAA SVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
DB 61 GKGPWVGFI RNKPNGGTTEYAA SVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
QY 121 YISHCRGVGYG YGFEFWGQALVTVSSASTKGPSVFLPAPSSKTSGGTAAALGCLVKDY 180
DB 121 YISHCRGVGYG YGFEFWGQALVTVSSASTKGPSVFLPAPSSKTSGGTAAALGCLVKDY 180

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:07:34 ; Search time 21.0061 Seconds
(without alignments)
2188.349 Million cell updates/sec

Title: US-09-758-173-8

Perfect score: 2561

Sequence: 1 MGWSLLFLFVAVTRVQCE.....MHEALNHVTKXSLSPCK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR76:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	68.8	330	GHU	Ig gamma-1 chain C
2	1626.5	63.5	377	A23511	Ig gamma-3 chain C
3	1624.5	63.4	377	A60764	Ig gamma-3 chain C
4	1600	62.5	326	G2HU	Ig gamma-2 chain C
5	1586.5	61.9	327	G4HU	Ig gamma-4 chain C
6	1494.5	58.4	444	P04436	monoclonal antibody
7	1478	57.7	470	S22080	Ig heavy chain pre
8	1467.5	57.3	469	S37483	Ig gamma-2a chain
9	1429	55.8	472	S31459	Ig gamma-1 chain -
10	1415	55.3	374	S69339	Ig heavy chain V r
11	1415	55.3	446	S40295	Ig gamma-2a chain
12	1392	54.4	474	G2MS11	Ig gamma-2b chain
13	1338.5	52.3	475	S01321	Ig gamma-2b chain
14	1259	49.2	328	I47159	Ig gamma 2a chain C
15	1256	49.0	255	S31866	Ig gamma 2b chain C
16	1253	48.9	328	I47160	Ig gamma 2b chain C
17	1250	48.8	234	P07207	Ig gamma chain C r
18	1227	47.9	328	I47158	Ig gamma 1 chain C
19	1225.5	47.9	323	GHRB	Ig gamma chain C r
20	1223	47.8	328	I47161	Ig gamma 3 chain C
21	1212.5	47.3	329	I G2GP	Ig gamma-2 chain C r
22	1157.5	45.2	308	C30554	Ig heavy chain C r
23	1152	45.0	289	G3HUW1	Ig gamma-3 heavy C
24	1148	44.8	326	P50017	Ig gamma-1 chain C
25	1142.5	44.6	333	P50018	Ig gamma-2b chain C
26	1138	44.4	324	G1MS	Ig gamma-1 chain C
27	1137	44.4	329	I G3MSC	Ig gamma-3 chain C
28	1133	44.2	393	I G1MS	Ig gamma-1 chain C
29	1126	44.0	398	I G3MS	Ig gamma-3 chain C

30 1122 43.8 330 1 G2MSA
31 1119.5 43.7 335 1 G2MSAB
32 1117 43.6 399 1 G2MSAM
33 1114.5 43.5 329 2 S00847
34 1108 43.3 322 2 PS0019
35 1088.5 42.5 327 2 S06611
36 1080 42.2 405 1 G2MSBM
37 1062 41.5 277 2 I47162
38 1009 39.4 548 2 S38864
39 863.5 33.7 549 2 S04845
40 829.5 32.4 249 2 S69340
41 797.5 31.1 572 2 B45529
42 797 31.1 220 2 A43444
43 771 30.1 627 2 S14683
44 758.5 29.6 241 2 S69131
45 739 28.9 218 2 A36040

330 1 G2MSA
335 1 G2MSAB
399 1 G2MSAM
329 2 S00847
322 2 PS0019
327 2 S06611
405 1 G2MSBM
277 2 I47162
548 2 S38864
549 2 S04845
249 2 S69340
572 2 B45529
220 2 A43444
627 2 S14683
241 2 S69131
218 2 A36040

Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2c chain
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma 4 chain c
Ig epsilon chain C
Ig heavy chain pre
Ig heavy chain VHI
Ig y heavy chain (c
Ig gamma-1 heavy c
Ig mu chain precu
Ig heavy chain (DO
Ig heavy chain V-I

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999

C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the Glm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

```

igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein N1e
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 9/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-205/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-304,250-304/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 68.8%; Score 1763; DB 1; Length 330;
Best Local Similarity 99.7%; Pred. No. 3e-97; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 1;

QY 149 ASTKGPSVFPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208
DB 1 ASTKGPSVFPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 209 GLYSLSSVTVPSVSSSLGTQTYICNVNHNKPSNTKVDKAPKSCDTHTCPCPAPPELLGG 268
DB 61 GLYSLSSVTVPSVSSSLGTQTYICNVNHNKPSNTKVDKAPKSCDTHTCPCPAPPELLGG 120

QY 269 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKREEQYN 328
DB 121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKREEQYN 180

QY 329 STYRVSVLTVLHODWLNGKEYCKVSKNKPAPLPIETKISKAGQPREPQVYTLPPSRDE 388
DB 181 STYRVSVLTVLHODWLNGKEYCKVSKNKPAPLPIETKISKAGQPREPQVYTLPPSRDE 240

QY 389 LTKNOVSLCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 448
DB 241 LTKNOVSLCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 449 QGQNVFSCSVHMLAHNHTQKSLSPGK 478
DB 301 QGQNVFSCSVHMLAHNHTQKSLSPGK 330

```

```

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; MID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 1626.5; DB 2; Length 377;
Best Local Similarity 81.7%; Pred. No. 4.1e-89;
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;

QY 149 ASTKGPSVFPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208
DB 1 ASTKGPSVFPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 209 GLYSLSSVTVPSVSSSLGTQTYICNVNHNKPSNTKVDKKA----- 246
DB 61 GLYSLSSVTVPSVSSSLGTQTYICNVNHNKPSNTKVDKVELKTPGLDTTHTCPCPEPKSC 120

QY 247 -----EPKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDT 281
DB 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKPKDT 180

QY 282 LMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKREEQYNSTYRVSVLTVLH 341
DB 181 LMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKREEQYNSTYRVSVLTVLH 240

QY 342 QDWLNGKEYCKVSKNKPAPLPIETKISKAGQPREPQVYTLPPSRDELTKNOVSLCLVK 401
DB 241 QDWLNGKEYCKVSKNKPAPLPIETKISKAGQPREPQVYTLPPSRDELTKNOVSLCLVK 300

QY 402 GFPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVHME 461
DB 301 GFPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVHME 360

QY 462 ALHNHTQKSLSPGK 478
DB 361 ALHNHTQKSLSPGK 377

RESULT 3
A50764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A50764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 conv
A:Reference number: A50764; MUID:90007613; PMID:2571587
A:Accession: A50764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 13.1847 Seconds
(without alignments)
1704.917 Million cell updates/sec

Title: US-09-758-173-8
Perfect score: 2561
Sequence: 1 MGWLLFLVAVATVQCE.....MHEALHNYTKSLSPGK 478

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	68.8	330	1 GC1_HUMAN	P01857 homo sapien
2	1600	62.5	326	1 GC2_HUMAN	P01859 homo sapien
3	1586.5	61.9	327	1 GC4_HUMAN	P01861 homo sapien
4	1326.5	47.9	323	1 GC_RABIT	P01870 oryctolagus
5	1212.5	47.3	329	1 GC2_CAVPO	P01862 cavia porce
6	1157	45.2	290	1 GC3_HUMAN	P01860 homo sapien
7	1148	44.8	326	1 GC1_RAT	P20759 rattus norv
8	1142.5	44.6	333	1 GCB_RAT	P20761 rattus norv
9	1138	44.4	324	1 GC1_MOUSE	P01868 mus musculus
10	1137	44.4	329	1 GC3_MOUSE	P22436 mus musculus
11	1133	44.2	393	1 GC3M_MOUSE	P01869 mus musculus
12	1146	44.0	398	1 GC3M_MOUSE	P03987 mus musculus
13	1142	43.8	330	1 GCRA_MOUSE	P01863 mus musculus
14	1119.5	43.7	335	1 GCAB_MOUSE	P01864 mus musculus
15	1117	43.6	399	1 GCAM_MOUSE	P01865 mus musculus
16	1114.5	43.5	329	1 GCC_RAT	P20762 rattus norv
17	1108	43.3	322	1 GCA_RAT	P20760 rattus norv
18	1085	42.4	336	1 GCB_MOUSE	P01866 mus musculus
19	1080	42.2	405	1 GCB_MOUSE	P01867 mus musculus
20	489	19.1	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	18.9	429	1 EPC_RAT	P01855 rattus norv
22	465	18.2	421	1 EPC_MOUSE	P06336 mus musculus
23	448	17.5	455	1 MUC_MOUSE	P01872 mus musculus
24	442	17.3	142	1 HV01_RAT	P01805 rattus norv
25	442	17.3	454	1 MUC_HUMAN	P01871 homo sapien
26	438	17.1	476	1 MUCM_MOUSE	P01873 mus musculus
27	437	17.1	458	1 MUC_RABIT	P03988 oryctolagus
28	430	16.8	144	1 HV26_MOUSE	P01795 mus musculus
29	427	16.7	479	1 MUCM_RABIT	P04221 oryctolagus
30	425	16.6	457	1 MUC_SUNMU	P20768 sunicus muri
31	420	16.4	450	1 MUC_CANFA	P01874 canis famil
32	419	16.4	123	1 HV28_MOUSE	P01787 mus musculus
33	418.5	16.3	122	1 HV20_MOUSE	P01789 mus musculus

ALIGNMENTS

RESULT 1
GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RT Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Pongstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884594;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.

34 418 16.3 123 1 HV19_MOUSE P01788 mus musculus
35 416.5 16.3 122 1 HV21_MOUSE P01790 mus musculus
36 415.5 16.2 117 1 HV17_MOUSE P01786 mus musculus
37 415.5 16.2 454 1 MUC_MESAU P06337 mesocricetu
38 415 16.2 123 1 HV22_MOUSE P01791 mus musculus
39 410 16.0 123 1 HV23_MOUSE P01792 mus musculus
40 403 15.7 391 1 MUCB_HUMAN P04220 homo sapien
41 399 15.6 123 1 HV25_MOUSE P01794 mus musculus
42 397 15.5 117 1 HV3C_HUMAN P01764 homo sapien
43 397 15.5 123 1 HV24_MOUSE P01793 mus musculus
44 396 15.5 115 1 HV32_MOUSE P01801 mus musculus
45 394 15.4 438 1 HVCS_HETFR P23087 heterodontu

RT Intrachain disulfide bonds";
 RL Biochemistry 9:3188-3196(1970).
 [7]
 RN DISULFIDE BONDS.
 RP MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 [8]
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RP MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RL aureus at 2.9- and 2.8-A resolution";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
 CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
 CC MARKER & THE G1M (NON-1) MARKERS.
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR PDB; 1AJ7; 12-NOV-97.
 DR PDB; 1DSB; 09-FEB-00.
 DR PDB; 1DSI; 09-FEB-00.
 DR PDB; 1DSV; 04-OCT-00.
 DR PDB; 1DN2; 17-MAY-00.
 DR PDB; 1EAK; 06-JUN-01.
 DR PDB; 1FCC; 20-JUL-95.
 DR PDB; 1H2H; 12-JUN-02.
 DR PDB; 1I7Z; 08-AUG-01.
 DR PDB; 1IIS; 16-MAY-01.
 DR PDB; 1IIX; 16-MAY-01.
 DR PDB; 1L6X; 10-APR-02.
 DR PDB; 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MTM; 147100;
 DR GO; 0005624; C:membrane fraction; NAS.
 DR GO; 0003823; F:antigen binding activity; TAS.
 DR GO; 0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGH1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 99 98 CH1.
 FT DOMAIN 110 110 HINGE.
 FT DOMAIN 111 223 CH2.

DOMAIN	224	330	CH3.
DISULFID	27	83	INTERCHAIN (WITH LIGHT CHAIN).
DISULFID	103	103	INTERCHAIN (WITH HEAVY CHAIN).
DISULFID	109	109	INTERCHAIN (WITH HEAVY CHAIN).
DISULFID	112	112	INTERCHAIN (WITH HEAVY CHAIN).
DISULFID	144	204	
DISULFID	250	308	N-LINKED (GLCNAC. . .).
CARBOHYD	180	180	REMOVED POST-TRANSLATIONALLY.
MOD_RES	330	330	K -> R (IN GIM(3) MARKER).
VARIANT	97	97	/FTID=VAR_003886.
VARIANT	239	239	D -> E (IN GIM(NON-1) MARKER).
VARIANT	241	241	/FTID=VAR_003887.
VARIANT	241	241	L -> M (IN GIM(NON-1) MARKER).
STRAND	122	126	/FTID=VAR_003888.
HELIX	130	134	
TURN	136	137	
STRAND	141	147	
STRAND	157	162	
TURN	163	164	
STRAND	165	166	
TURN	168	171	
STRAND	176	179	
TURN	180	181	
STRAND	182	190	
HELIX	193	197	
TURN	198	199	
STRAND	202	207	
TURN	209	210	
STRAND	215	219	
STRAND	227	227	
STRAND	230	234	
HELIX	238	242	
STRAND	245	256	
STRAND	260	265	
STRAND	270	270	
STRAND	274	276	
STRAND	280	281	
TURN	283	284	
STRAND	287	296	
HELIX	297	301	
TURN	302	303	
STRAND	305	312	
TURN	313	314	
TURN	316	317	
STRAND	320	325	
SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 68.8%; Score 1763; DB 1; Length 330;
 Best Local Similarity 99.7%; Pred. No. 1.2e-117;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	149	ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPEPTVTSWNSGALTSGVHTFPAVLQSS	208
DB	1	ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPEPTVTSWNSGALTSGVHTFPAVLQSS	60
QY	209	GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKYDKKAEKSCDKTHTCCPCAPPELLGG	268
DB	61	GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKYDKKAEKSCDKTHTCCPCAPPELLGG	120
QY	269	PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKRREQYN	328
DB	121	PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKRREQYN	180
QY	329	STYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	388
DB	191	STYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	240
QY	389	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRW	448
DB	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRW	300

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2178.5	85.1	471	4	Q8TC77	Q8TC77 homo sapien
2	2103.5	82.1	521	1	Q8N4Y9	Q8N4Y9 homo sapien
3	1838	71.8	473	4	Q8TC63	Q8TC63 homo sapien
4	1632.5	63.7	469	11	Q8R3V9	Q8R3V9 mus musculu
5	1612.5	63.0	509	4	Q8NF17	Q8NF17 homo sapien
6	1495.5	58.4	473	11	Q9D8L4	Q9D8L4 mus musculu
7	1480.5	57.8	473	11	Q91Z05	Q91Z05 mus musculu
8	1480	57.8	468	11	Q99L31	Q99L31 mus musculu
9	1472.5	57.5	473	11	Q99L25	Q99L25 mus musculu
10	1469.5	57.4	437	11	Q9R1A4	Q9R1A4 mus musculu
11	1458.5	57.0	463	11	Q99LC4	Q99LC4 mus musculu
12	1435	55.3	474	11	Q8R3K6	Q8R3K6 mus musculu
13	1268	49.5	701	4	Q96PQ8	Q96PQ8 homo sapien
14	1262.5	49.3	337	6	Q95M34	Q95M34 equus cabal
15	879.5	34.3	597	4	Q96BB9	Q96BB9 homo sapien
16	845.5	33.0	499	4	Q8N5K4	Q8N5K4 homo sapien


```
QY 122 ISHCRGGYCYGTEFWGQALVTYSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYF 181
Db 126 -----WYFDLMRGGLVTVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYF 174
QY 182 PEPVTVSNWNSGALTSVHTFPFAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTK 241
Db 175 PEPVTVSNWNSGALTSVHTFPFAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTK 234
QY 242 VDKKAEPKSCDTHTCPCPAPELLGGPSVFLFPKPKDLMISRTPEVTCVVDVSHED 301
Db 235 VDKKVEPKSCDTHTCPCPAPELLGGPSVFLFPKPKDLMISRTPEVTCVVDVSHED 294
QY 302 PEVFNFWYDVGVEVENAKTKPREEQYNSTYRWVSVLTVLHODWLNGLNGKEYCKVSNKALPA 361
Db 295 PEVFNFWYDVGVEVENAKTKPREEQYNSTYRWVSVLTVLHODWLNGLNGKEYCKVSNKALPA 354
QY 362 PIEKTIKAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENN 421
Db 355 PIEKTIKAKQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENN 414
QY 422 YKTPPVLDSDGSPFLYKLVDRKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 478
Db 415 YKTPPVLDSDGSPFLYKLVDRKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 471
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RESULT 2

```
Q8N4Y9
ID Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig-CL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGLIKE; 3.
DR PROSITE; PS00290; IGMHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D2D2E72D6CA2 CRC64;
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Query Match 82.1%; Score 2103.5; DB 4; Length 521;
Best Local Similarity 76.4%; Pred. No. 5.1e-174;
Matches 401; Conservative 27; Mismatches 42; Indels 55; Gaps 3;
QY 1 MWSLILLFLAVATRVCEVQLVESGGGLVQPGSLRYSCAVSG--FTFSDHYMYWFRQAP 60
Db 5 LSWLLLVVFLQG-----VQCEVOLVDSGGGLVQPGSLRYSCAVSGFTFSDHYMYWFRQAP 60
QY 61 GKPEWGFIRKPNKGTTTEYAASVKDRFTISRDSKSIAYLQMSLKIEDTAVYYCTTS 120
Db 61 GKPEWGFIRKPNKGTTTEYAASVKDRFTISRDSKSIAYLQMSLKIEDTAVYYCTTS 117
QY 121 YISHCRGGYCYGTEFWGQALVTYSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDY 180
Db 118 -VRDLEGAGKYDWFIDWGRGILVTYSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDY 176
QY 181 PEPVTVSNWNSGALTSVHTFPFAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNT 240
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Db 177 PEPVTVSNWNSGALTSVHTFPFAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNT 236
QY 241 KVDKKA-----EPKSCDK 253
Db 237 KVDKRVELKTLPGDTTHTCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDT 296
QY 254 THTCPCPAPELLGGPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDVG 313
Db 297 PPCPCPAPELLGGPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDVG 356
QY 314 EVENAKTKPREEQYNSTYRWVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIETKISAKQ 373
Db 357 EVENAKTKPREEQYNSTYRWVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIETKISAKQ 416
QY 374 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNKTTPPVLDSDG 433
Db 417 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNKTTPPVLDSDG 476
QY 434 SPFLYKLVDRKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 478
Db 477 SPFLYKLVDRKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 521
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RESULT 3

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Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IGLIKE; 4.
DR PROSITE; PS00290; IGMHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
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Query Match 71.8%; Score 1838; DB 4; Length 473;
Best Local Similarity 75.5%; Pred. No. 5.1e-151;
Matches 357; Conservative 33; Mismatches 67; Indels 16; Gaps 4;
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Db 15 LLLVAPRWVLSRLQIQESGPGLLKPSVTLTCTVSGDSVASSSYWGWVRQPGKGL 74
QY 66 WGFINKPNKGTTTEYAASVKDRFTISRDSKSIAYLQMSLKIEDTAVYYCTTSYISHC 125
Db 75 WIGTIN---FSGNNYSPSLRSRTVMSADMSSENFYKLKDSVTAADATVYYCAAGHL--- 128
QY 126 RGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 185
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QY 186 TVSNWNSGALTSVHTFPFAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTKVDK 245
Db 184 TVSNWNSGALTSVHTFPFAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTKVDK 243
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 09:12:09 ; Search time 21.2295 Seconds
(without alignments)
952.662 Million cell updates/sec

Title: US-09-758-173-8
Perfect score: 2561
Sequence: 1 MGWSLLFLVAVATRVQCE.....MHEALNNHYTKSLSPGK 478

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2.6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	2184.5	85.3	452	4	US-09-234-340A-71
7	2146.5	83.8	449	4	US-09-679-397-2
8	2146.5	83.8	449	4	US-09-680-148-2
9	2146.5	83.8	449	4	US-09-304-465A-2
10	2138.5	83.5	459	1	US-08-157-101A-7
11	2135	83.4	451	2	US-08-887-352B-18
12	2135	83.4	451	3	US-09-109-207C-18
13	2135	83.4	451	3	US-09-282-505-2
14	2135	83.4	451	3	US-09-054-255-2
15	2135	83.4	451	3	US-09-296-005-18
16	2135	83.4	451	4	US-09-282-846-2
17	2135	83.4	451	4	US-09-680-145-2
18	2132	83.2	451	2	US-08-887-352B-14
19	2132	83.2	451	3	US-08-887-352B-16
20	2132	83.2	451	3	US-08-466-151-65
21	2132	83.2	451	3	US-09-109-207C-14
22	2132	83.2	451	3	US-09-109-207C-16
23	2132	83.2	451	3	US-09-296-005-14
24	2132	83.2	451	3	US-09-296-005-16
25	2132	83.2	453	3	US-08-466-151-8
26	2132	83.2	453	3	US-08-466-163B-8
27	2100	82.0	476	2	US-08-378-939-10

28	2089.5	81.6	467	3	US-09-049-672A-8	Sequence 8, Appli
29	2078	81.1	472	4	US-08-793-450-8	Sequence 8, Appli
30	2073.5	81.0	475	4	US-09-740-002-25	Sequence 25, Appli
31	2073	80.9	476	3	US-08-487-550-4	Sequence 4, Appli
32	2073	80.9	476	4	US-09-526-098-4	Sequence 4, Appli
33	2071.5	80.9	475	4	US-09-740-002-27	Sequence 27, Appli
34	2069	80.8	449	1	US-08-458-516-13	Sequence 13, Appli
35	2064	80.6	472	4	US-09-301-593-43	Sequence 43, Appli
36	2058.5	80.4	467	1	US-08-704-744-81	Sequence 81, Appli
37	2056.5	80.3	446	3	US-08-397-411-7	Sequence 7, Appli
38	2054	80.2	468	4	US-09-485-737B-67	Sequence 67, Appli
39	2054	80.2	472	4	US-09-301-593-30	Sequence 30, Appli
40	2054	80.2	711	4	US-08-485-737B-90	Sequence 90, Appli
41	2053	80.2	476	3	US-08-487-550-12	Sequence 12, Appli
42	2053	80.2	476	4	US-09-526-098-12	Sequence 12, Appli
43	2046.5	79.9	473	3	US-09-049-672A-4	Sequence 4, Appli
44	2040.5	79.7	552	5	PCT-US93-07832-23	Sequence 23, Appli
45	2037.5	79.6	469	2	US-07-934-373C-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1
US-08-487-550-8
; Sequence 8, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-8

Query Match 100.0%; Score 2561; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e-198;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GKGPEWVGFIRKNGGTTTEAASVKDRFTISRDDSKSIAYLQMSLKIETDVAIYCTTS 120
QY 121 YISCRGGVCGYGGYFEGWGGALVTSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDY 180
Db 121 YISCRGGVCGYGGYFEGWGGALVTSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDY 180
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Db 181 FPEPVTVSNWNGALTSVGHVTFPAVLQSSGLYSSVVTVPSSSLGTQTYICNVNHPKPSNT 240
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Db 241 KVDKKAEPKSCDKTHTCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVDSHE 300
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; Sequence 8, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/526,098
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-526-098-8
Query Match 100.0%; Score 2561; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e-198;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGSLLTLLFLVAVATVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHMYWYFRAP 60
QY 61 GKGPEWVGFIRKNGGTTTEAASVKDRFTISRDDSKSIAYLQMSLKIETDVAIYCTTS 120
Db 61 GKGPEWVGFIRKNGGTTTEAASVKDRFTISRDDSKSIAYLQMSLKIETDVAIYCTTS 120
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Db 121 YISCRGGVCGYGGYFEGWGGALVTSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDY 180
QY 181 FPEPVTVSNWNGALTSVGHVTFPAVLQSSGLYSSVVTVPSSSLGTQTYICNVNHPKPSNT 240
Db 181 FPEPVTVSNWNGALTSVGHVTFPAVLQSSGLYSSVVTVPSSSLGTQTYICNVNHPKPSNT 240
QY 241 KVDKKAEPKSCDKTHTCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVDSHE 300
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RESULT 3
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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421.442 Million cell updates/sec

Title: US-09-758-173-8
Perfect score: 2561
Sequence: 1 MGWSLLFLVAVATRYQCE.....MHEALHNYTKSLSPGK 478

Scoring table: BLOSUM62

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Post-processing: Minimum Match 0%

Maximum Match 100%

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2561	100.0	478	12	US-10-251-532-8
4	2561	100.0	478	14	US-10-124-905-8
5	2184.5	85.3	452	11	US-09-726-258-71
6	2183	85.2	474	12	US-10-225-108A-3
7	2183	85.2	474	12	US-09-848-832-3
8	2176	85.0	470	15	US-10-020-786-9
9	2176	85.0	470	15	US-10-227-694-5
10	2160	84.3	451	10	US-09-822-698A-26
11	2156	84.2	476	15	US-10-020-786-11
12	2154	84.1	449	10	US-09-736-371B-21
13	2149.5	83.9	731	10	US-09-825-012-46
14	2149.5	83.9	741	10	US-09-825-012-55
15	2146.5	83.8	449	12	US-10-356-974-2

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Sequence 2, Appli
Sequence 52, Appli
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Sequence 145, App
Sequence 68, Appli
Sequence 143, App
Sequence 143, App
Sequence 117, App

16 2146.5 83.8 449 15 US-10-253-366-2
17 2146.5 83.8 449 15 US-10-316-694-2
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19 2144.5 83.7 739 10 US-09-825-012-61
20 2138.5 83.5 730 10 US-09-825-012-49
21 2138.5 83.5 740 10 US-09-825-012-58
22 2137.5 83.5 444 15 US-10-150-475A-6
23 2135 83.4 451 9 US-09-920-171-18
24 2135 83.4 451 12 US-10-113-996-18
25 2135 83.4 451 12 US-10-292-869-2
26 2135 83.4 451 12 US-09-792-938-2
27 2135 83.4 470 12 US-10-384-933-157
28 2135 83.4 470 15 US-10-216-484-157
29 2132 83.2 451 9 US-09-920-171-14
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31 2132 83.2 451 11 US-09-925-179-65
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33 2132 83.2 451 12 US-10-113-996-16
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35 2132 83.2 453 9 US-09-802-096-8
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37 2129 83.1 451 11 US-09-925-179-66
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42 2122 82.9 451 11 US-09-925-179-68
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ALIGNMENTS

RESULT 1
US-09-948-429B-8
; Sequence 8, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620

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; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-8

Query Match      100.0%; Score 2561; DB 10; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e-169;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGWSLLILFLVAVATRVQCEVQLVQVGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60
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DB 61 GKGPWVGFIIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
QY 121 YISHCRGGVCGYGFYFVWGQALVTVSSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDY 180
DB 121 YISHCRGGVCGYGFYFVWGQALVTVSSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDY 180
QY 181 FPEPTVSNWNSGALTSVHTFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 240
DB 181 FPEPTVSNWNSGALTSVHTFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 240
QY 241 KYDKKAEPKSCDKTHTCPPELPGPSVFLPPPKPKDTLMSRTPETVTVVVDVSH 300
DB 241 KYDKKAEPKSCDKTHTCPPELPGPSVFLPPPKPKDTLMSRTPETVTVVVDVSH 300
QY 301 DPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYCKKVSNNKALP 360
DB 301 DPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYCKKVSNNKALP 360
QY 361 APIEKTISKAKGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPEN 420
DB 361 APIEKTISKAKGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPEN 420
QY 421 NYKTPPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 478
DB 421 NYKTPPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 478

RESULT 2
US-10-124-807-8
; Sequence 8, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMARIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-807-8

Query Match      100.0%; Score 2561; DB 12; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e-169;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLLILFLVAVATRVQCEVQLVQVGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60
DB 1 MGWSLLILFLVAVATRVQCEVQLVQVGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60
QY 61 GKGPWVGFIIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
DB 61 GKGPWVGFIIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTS 120
QY 121 YISHCRGGVCGYGFYFVWGQALVTVSSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDY 180
DB 121 YISHCRGGVCGYGFYFVWGQALVTVSSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDY 180
QY 181 FPEPTVSNWNSGALTSVHTFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 240
DB 181 FPEPTVSNWNSGALTSVHTFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNT 240
QY 241 KYDKKAEPKSCDKTHTCPPELPGPSVFLPPPKPKDTLMSRTPETVTVVVDVSH 300
DB 241 KYDKKAEPKSCDKTHTCPPELPGPSVFLPPPKPKDTLMSRTPETVTVVVDVSH 300
QY 301 DPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYCKKVSNNKALP 360
DB 301 DPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYCKKVSNNKALP 360
QY 361 APIEKTISKAKGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPEN 420
DB 361 APIEKTISKAKGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPEN 420
QY 421 NYKTPPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 478
DB 421 NYKTPPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 478

RESULT 3
US-10-291-532-8
; Sequence 8, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; COMBINATION WITH OTHER THERAPIES
; TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 ; Search time 1867.6 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-9
Perfect score: 711
Sequence: 1 ATGAGGGTCCCGCTCAGCT.....CCCCTACAGATGTTTCATGA 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
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- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_fod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	711	100.0	711	6	AR108866	AR108866 Sequence
2	711	100.0	711	6	AR265200	AR265200 Sequence
3	711	100.0	711	6	BD063038	BD063038 Identific
4	582.6	81.9	935	6	AR135362	AR135362 Sequence
5	575.4	80.9	790	9	AB064208	AB064208 Homo sapi
6	573	80.6	870	6	BD176841	BD176841 A method
7	573	80.6	870	9	HSIGLV	XI4583 Human mRNA
8	571.2	80.3	903	9	BC020233	BC020233 Homo sapi
9	570.6	80.3	827	9	AB064143	AB064143 Homo sapi
10	566.6	79.7	800	9	AB064188	AB064188 Homo sapi
11	566.4	79.7	919	9	BC022098	BC022098 Homo sapi
12	566	79.6	815	9	AB064149	AB064149 Homo sapi
13	562.8	79.2	816	9	AB064148	AB064148 Homo sapi
14	562.4	79.1	827	9	AB064147	AB064147 Homo sapi
15	562.2	79.1	827	9	AB064219	AB064219 Homo sapi
16	562.2	79.1	750	9	HSIGVL027	X57817 Human rear
17	560	78.8	747	9	HSIGVL006	X57806 Human rear
18	558	78.5	821	9	AB064141	AB064141 Homo sapi
19	558	78.5	824	9	AB064227	AB064227 Homo sapi
20	557.6	78.4	804	9	AB064172	AB064172 Homo sapi
21	556.4	78.3	790	9	AB064206	AB064206 Homo sapi
22	556.4	78.3	824	9	AB064226	AB064226 Homo sapi
23	555.4	78.1	827	9	HSIGVL021	X57811 Human rear
24	554.8	78.0	816	9	AB064150	AB064150 Homo sapi
25	554.4	78.0	790	9	AB064169	AB064169 Homo sapi
26	554.4	78.0	803	9	AB064166	AB064166 Homo sapi
27	553.2	77.8	829	9	AB064203	AB064203 Homo sapi
28	552.8	77.7	788	9	AB064171	AB064171 Homo sapi
29	552.8	77.7	789	9	AB064170	AB064170 Homo sapi
30	552.8	77.7	819	9	AB064151	AB064151 Homo sapi
31	552.6	77.7	768	6	BD078409	BD078409 Antigen-b
32	552.6	77.7	768	6	BD078410	BD078410 Antigen-b
33	551.6	77.6	781	9	AB064216	AB064216 Homo sapi
34	550	77.4	828	9	AB064222	AB064222 Homo sapi
35	548.4	77.1	827	9	AB064218	AB064218 Homo sapi
36	548.4	77.1	831	9	AB064224	AB064224 Homo sapi
37	547.8	77.0	802	9	HSIGVL032	X57822 Human rear
38	546.2	76.8	810	9	HSIGVL025	X57815 Human rear
39	546.2	76.8	816	9	AB064178	AB064178 Homo sapi
40	545.6	76.7	9472	6	AX287808	AX287808 Sequence
41	545	76.7	789	9	AB064205	AB064205 Homo sapi
42	541	76.1	927	9	BC012876	BC012876 Homo sapi
43	540.8	76.0	648	9	AF191795	AF191795 Homo sapi
44	540.4	76.0	824	9	AB064228	AB064228 Homo sapi
45	540.2	76.0	705	6	AR108862	AR108862 Sequence

ALIGNMENTS

RESULT 1
AR108866
LOCUS AR108866 711 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6113898.
ACCESSION AR108866
VERSION AR108866.1 GI:12825142
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 711)
AUTHORS Anderson,D.R., Brams P., Hanna N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
JOURNAL Patent: US 6113898-A 9 05-SEP-2000;

FEATURES	Location/Qualifiers
source	1..711
BASE COUNT	160 a 226 c 193 g 132 t
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Query Match	100.0%; Score 711; DB 6; Length 711;
Best Local Similarity	100.0%; Pred. No. 5.8e-174;
Matches 711; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTGCTCTGCTCTGGCTCCGAGGTGCACGATGT 60
DB	1 ATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTGCTCTGCTCTGGCTCCGAGGTGCACGATGT 60
QY	61 GAGTCTGTCTGTACACAGCGCCCTCAGTCTCTGGGGCCCGAGGCGAGAAGGTCAACCATC 120
DB	61 GAGTCTGTCTGTACACAGCGCCCTCAGTCTCTGGGGCCCGAGGCGAGAAGGTCAACCATC 120
QY	121 TCGTGCATCTGGAGACACTTCACATCTGGAGTTATGATCTACATTTGTACACAGAGCTC 180
DB	121 TCGTGCATCTGGAGACACTTCACATTTGGAGTTATGATCTACATTTGTACACAGAGCTC 180
QY	181 CCAGGAAGCGGCCCAAACTCCTCATCTATGACATTAAACAAGCGACCTTCAGGAATTCT 240
DB	181 CCAGGAAGCGGCCCAAACTCCTCATCTATGACATTAAACAAGCGACCTTCAGGAATTCT 240
QY	241 GACCGATTCTTGGCTCCAGTCTGGTACCGGGCCCTCCCTGGCCATCATCTGGGTCCAG 300
DB	241 GACCGATTCTTGGCTCCAGTCTGGTACCGGGCCCTCCCTGGCCATCATCTGGGTCCAG 300
QY	301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGGCTGAATGCTCAGGTA 360
DB	301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGGCTGAATGCTCAGGTA 360
QY	361 TTCGAGAGGGAGCCCGGCTGACCGTCTTAGTTCAGCCCAAGCGTGCCTCCGCTCACT 420
DB	361 TTCGAGAGGGAGCCCGGCTGACCGTCTTAGTTCAGCCCAAGCGTGCCTCCGCTCACT 420
QY	421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTGCTCATA 480
DB	421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTGCTCATA 480
QY	481 AGTGACTTCTACCCGGGAGCGGTGACAGTGGCTTGAAGCGAGTACGAGCCCGTCAAG 540
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QY	541 GCGGAGTGGAGACCCACACCCCTCCAAACAAGCAACAAGTACGCGGCCAGCAGC 600
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QY	601 TACCTGAGCCTGAGCGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTCAAG 660
DB	601 TACCTGAGCCTGAGCGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTCAAG 660
QY	661 CATGAAGGGAGCCCGTGGAGAAGACAGTGGCCCTTACAGAAATGTTATGA 711
DB	661 CATGAAGGGAGCCCGTGGAGAAGACAGTGGCCCTTACAGAAATGTTATGA 711
RESULT 2	
LOCUS	AR265200
DEFINITION	Sequence 9 from patent US 6492134.
ACCESSION	AR265200
VERSION	AR265200.1 GI:29693621
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 711)
AUTHORS	Aquin, S. and Vezina, Louis.-P.
TITLE	Method for producing polyhydroxyalkanoates in recombinant organisms
JOURNAL	Patent: US 6492134-A 9 10-DEC-2002;

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 12:12:30 ; Search time 145.625 Seconds
(without alignments)
13179.730 Million cell updates/sec

Title: US-09-758-173-9
Perfect score: 711
Sequence: 1 ATGAGGGTCCCGCTCAGCT.....CCCTACAGATGTTTCATGA 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552736 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	19	AAV35488
2	711	100.0	711	19	AAV35488
3	709.4	99.8	711	18	AAV35488
4	582.6	81.9	935	22	AAV35488
5	573	80.6	870	24	AAV35488
6	571.4	80.4	884	11	AAV35488
7	565.2	79.5	762	22	AAV35488
8	558.8	78.6	5679	22	AAV35488

9	552.6	77.7	758	20	AAV35488
10	552.6	77.7	758	20	AAV35488
11	547	76.9	654	14	AAV35488
12	546.2	76.8	810	23	AAV35488
13	545.6	76.7	9532	25	AAV35488
14	540.2	76.0	705	18	AAV35488
15	540.2	76.0	705	19	AAV35488
16	540.2	76.0	705	24	AAV35488
17	534.8	75.2	2112	24	AAV35488
18	533.2	75.0	651	19	AAV35488
19	533.2	75.0	708	22	AAV35488
20	532.2	74.9	915	24	AAV35488
21	532.2	74.9	915	24	AAV35488
22	532.2	74.9	915	24	AAV35488
23	532.2	74.9	915	24	AAV35488
24	530.2	74.6	895	22	AAV35488
25	527.6	74.2	705	25	AAV35488
26	523.6	73.6	708	22	AAV35488
27	522.8	73.5	1845	24	AAV35488
28	518.8	73.0	708	22	AAV35488
29	510.6	71.8	891	22	AAV35488
30	509.2	71.6	763	23	AAV35488
31	502.6	70.7	902	14	AAV35488
32	499.4	70.2	889	23	AAV35488
33	498.6	70.1	906	22	AAV35488
34	496.4	69.8	951	23	AAV35488
35	494.4	69.5	783	23	AAV35488
36	494.4	69.5	876	23	AAV35488
37	493.8	69.5	888	21	AAV35488
38	487.4	68.6	1636	23	AAV35488
39	487.4	68.6	1636	23	AAV35488
40	486.6	68.4	756	23	AAV35488
41	484.2	68.1	885	19	AAV35488
42	484.2	68.1	885	24	AAV35488
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44	484.2	68.1	885	25	AAV35488
45	482.8	67.9	702	24	AAV35488

ALIGNMENTS

RESULT 1
AAV35488
ID AAV35488 standard; DNA; 711 BP.

XX AAV35488;
XX AC
XX 29-SEP-1998 (first entry)
XX Macaque primatized 16C10 light chain DNA.
XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
XX CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
XX T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
XX immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
XX T cell proliferation; ss.
XX Macaca fascicularis.

Key	Location/Qualifiers
FT CDS	1..711
FT	/*tag= a
FT	/product= 16C10 light chain
XX	WO9819706-A1.
XX	14-MAY-1998.
XX	29-OCT-1997; 97WO-US19906.
XX	08-NOV-1996; 96US-0746361.

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:05:20 ; Search time 1175.83 Seconds
(without alignments)
14696.420 Million cell updates/sec

Title: US-09-758-173-9

Perfect score: 711

Sequence: 1 ATGAGGTCCTCCGCTCAGCT.....CCCTACAGATGTCATGA 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3:	em_estlin:**
4:	em_estmu:**
5:	em_estov:**
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8:	em_htc:**
9:	gb_est1:**
10:	gb_est2:**
11:	gb_htc:**
12:	gb_est3:**
13:	gb_est4:**
14:	gb_est5:**
15:	em_estfun:**
16:	em_estom:**
17:	em_gss_hum:**
18:	em_gss_inv:**
19:	em_gss_pln:**
20:	em_gss_vrt:**
21:	em_gss_fun:**
22:	em_gss_mam:**
23:	em_gss_mus:**
24:	em_gss_pro:**
25:	em_gss_rod:**
26:	em_gss_pbg:**
27:	em_gss_vrl:**
28:	gb_gss1:**
29:	gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569.2	80.1	956	13	BQ711292
2	562.6	79.1	913	13	BQ708635
3	559	78.6	894	13	BQ708570
4	558.6	78.6	819	10	BG685644

5	557.8	78.5	873	13	BQ712653
6	556	78.2	701	14	CB554359
7	555.6	78.1	755	10	BG755185
8	552.2	77.7	687	14	CB554445
9	552.2	77.7	1007	12	BM920020
10	552.2	77.7	1060	12	BM906351
11	551.6	77.6	910	10	BG757147
12	549.4	77.3	857	13	BQ80529
13	549	77.2	764	10	BG755548
14	546	76.8	817	12	B1835917
15	545.4	76.7	896	10	BG685967
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17	544.6	76.6	849	10	BG756887
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25	538.2	75.7	873	10	BG686011
26	537.4	75.6	935	10	BG755314
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ALIGNMENTS

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DEFINITION AGENCOURT_8353826 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278335
5', mRNA sequence.
ACCESSION BQ711292
VERSION BQ711292.1 GI:21850191
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 956)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM2466 row: c column: 08
High quality sequence start: 10

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:10:05 ; Search time 37.7874 Seconds
(without alignments)
8304.972 Million cell updates/sec

Title: US-09-758-173-9

Perfect score: 711

Sequence: 1 ARGAGGTCCTCCGCTCAGCT.....CCCTACAGAATGTTTCATGA 711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	3	US-08-487-550-9
2	711	100.0	711	4	US-09-526-098-9
3	582.6	81.9	935	3	US-09-049-672A-20
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5	540.2	76.0	705	4	US-09-526-098-1
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8	510.6	71.8	891	3	US-09-049-672A-23
9	502.6	70.7	902	2	US-08-378-939-11
10	484.2	68.1	885	4	US-09-152-060-47
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12	468.4	65.9	702	3	US-08-523-894-5
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34 306.2 43.1 771 4 US-09-062-451-241 Sequence 241, App
35 306.2 43.1 771 4 US-09-598-326-241 Sequence 241, App
36 306.2 43.1 771 4 US-09-289-198-241 Sequence 241, App
37 288.6 42.0 805 4 US-09-620-312D-62 Sequence 62, Appl
38 281.2 39.5 329 4 US-09-702-705-409 Sequence 409, App
39 281.2 39.5 329 4 US-09-736-457-409 Sequence 409, App
40 264.4 37.2 408 4 US-09-025-769B-169 Sequence 169, App
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42 254.8 35.8 933 4 US-09-079-029-8 Sequence 8, Appli
43 253.2 35.6 642 2 US-08-634-783A-4 Sequence 4, Appli
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45 246.8 34.7 346 2 US-08-761-277A-50 Sequence 50, Appl

ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..711
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..711
US-08-487-550-9

[illegible]

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; Sequence 9, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRYMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible

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1 OPERATING SYSTEM: PC-DOS/MS-DOS
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3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/526,098
5 FILING DATE:
6 CLASSIFICATION:
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 09/383,916
9 FILING DATE:
10 APPLICATION NUMBER: US 08/487,550
11 FILING DATE: 07-JUN-1995
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Teskin, Robin L.
14 REGISTRATION NUMBER: 35,030
15 REFERENCE/DOCKET NUMBER: 012712-131
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 703-836-6620
18 TELEFAX: 703-836-2021
19 INFORMATION FOR SEQ ID NO: 9:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 711 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: not relevant
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: 1..711
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QY	301	ACTGAGGAT	GAGGCTGATTTACTGCCAGTCCCTATGACAGCAGGCTGAATGCTCAGGTA	360
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QY	361	TTGCGAGG	AGGACCGGGCTGACCGTCCTAGGTGACGCCCAAGGCTGCCCTCGGTCACT	420
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QY	421	CTGTTC	CCGCCCTCCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTGCTCAT	480
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Copyright (c) 1993 - 2003 CompuGen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22	532.2	74.9	915	12	US-09-873-319-710	Sequence 710, App
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24	531.8	74.8	2635	14	US-10-198-846-13529	Sequence 13529, A
25	527.6	74.2	705	12	US-10-194-801C-3	Sequence 3, Appli
26	525.4	73.9	2635	14	US-10-198-846-13529	Sequence 13529, A
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30	494.6	69.6	1537	14	US-10-198-846-13540	Sequence 13540, A
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41	470.4	66.2	895	14	US-10-198-846-12838	Sequence 12838, A
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ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 27.6933 Seconds
(without alignments)
1352.654 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1232	100.0	236	19 AAW63764	Macaque primatized o
2	1232	100.0	236	23 AAU11645	Protein sequence o
3	1229	99.8	236	18 AAW01821	Primate anti-hu
4	1052.5	85.4	236	22 AAB36209	Human immune syste
5	1006	81.7	235	20 AAW8465	Monoclonal antibod
6	1001	81.2	236	22 AAG32083	Novel human diagno
7	999.5	81.1	221	23 ABE52959	Human lung specifi
8	992.5	80.6	214	24 ABR01470	Human anti-TIMP-1
9	989	80.3	213	24 ABR01468	Human anti-TIMP-1

10	989	80.3	213	24	ABR01475	Human anti-TIMP-1
11	987	80.1	268	23	ABP62895	Human polypeptide
12	981.5	79.7	214	24	ABR01467	Human anti-TIMP-1
13	979.5	79.5	217	14	AA44163	Anti-HIV-1 recombi
14	979	79.5	234	24	ABG73422	Human Igg anti-rhe
15	973	79.0	234	18	AAW01817	Primate anti-hu
16	973	79.0	234	19	AAW63760	Macaque primatized
17	973	79.0	234	23	AAU11538	Protein sequence o
18	971.5	78.9	217	19	AAW40533	Antibody HB4C5 lig
19	969	78.7	242	24	ABU08021	Monoclonal rabies
20	968.5	78.6	248	22	ABG26352	Novel human diagno
21	965	78.3	235	22	AA36212	Human immune syste
22	965	78.3	235	22	AA36214	Human immune syste
23	961.5	78.0	219	23	ABG80711	Antibody peptide co
24	958.5	77.8	216	24	ABR01477	Human anti-TIMP-1
25	958.5	77.8	236	22	ABG19293	Novel human diagno
26	957	77.7	235	22	AA64472	Human type antihum
27	957	77.7	614	23	ABB06275	Plasmid scFv/CC046
28	955	77.5	235	14	AA31024	Antibody D light c
29	954	77.4	215	24	ABR01476	Human anti-TIMP-1
30	952.5	77.3	214	24	ABR01487	Human anti-TIMP-1
31	951.5	77.2	216	24	ABR01473	Human anti-TIMP-1
32	951	77.2	215	24	ABR01463	Human anti-TIMP-1
33	950.5	77.2	214	24	ABR01490	Human anti-TIMP-1
34	950.5	77.2	216	24	ABR01488	Human anti-TIMP-1
35	950.5	77.2	219	21	AA30594	Variable and first
36	948.5	77.0	214	24	ABR01485	Human anti-TIMP-1
37	947.5	76.9	216	24	ABR01483	Human anti-TIMP-1
38	947	76.9	215	24	ABR01491	Human anti-TIMP-1
39	947	76.9	215	24	ABR01493	Human anti-TIMP-1
40	946	76.8	215	24	ABR01498	Human anti-TIMP-1
41	945.5	76.7	216	24	ABR01482	Human anti-TIMP-1
42	945	76.7	215	24	ABR01464	Human anti-TIMP-1
43	945	76.7	235	22	AA64474	Human type antihum
44	945	76.7	235	22	AA64476	Human type antihum
45	944	76.6	215	24	ABR01479	Human anti-TIMP-1

ALIGNMENTS

RESULT 1
AAW63764
ID AAW63764 standard; Protein; 236 AA.
XX
AC AAW63764;
XX
DT 29-SEP-1998 (first entry)
XX
DE Macaque primatized 16C10 light chain protein.
XX
KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation.
XX
OS Macaca fascicularis.
XX
PN WC9819706-A1.
XX
PD 14-MAY-1998.
XX
PF 29-OCT-1997; 97WO-US19906.
XX
PR 08-NOV-1996; 960S-0746361.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brans P, Hanna N;
XX
DR WPI; 1998-286601/25.
DR N-PSDB; AAV35488.

XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours
XX
XX
XX Example 7; Fig 5a; 87pp; English.
XX
XX This sequence represents a primatized form of the antibody 16C10 light
CC chain from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
XX Sequence 236 AA;

Query Match 100.0%; Score 1232; DB 19; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e-66;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRVPAQLLGLLLLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIGGYDLHWYQQL 60
DB 1 MRVPAQLLGLLLLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIGGYDLHWYQQL 60
QY 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYOSYSSSLNAQV 120
DB 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYOSYSSSLNAQV 120
QY 121 FGGGTRTLVGLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FGGGTRTLVGLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 181 AGVETTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 AGVETTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 2
AAU11645
ID AAU11645 standard; Protein; 236 AA.
XX AAU11645;
XX
XX 12-MAR-2002 (first entry)
XX
XX Protein sequence of primatized form of the light chain of 16C10 antibody.
DE
DE Human; macaque monkey; light chain; primatized antibody; 16C10 antibody;
KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW graft-vs-host disease; immunosuppression; organ rejection;
KW interleukin-2; IL-2; mutant; mutin.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Macaca sp.
OS Synthetic.
XX
XX WO2000189567-A1.

PD 29-NOV-2001.
XX
XX 22-MAY-2001; 2001WO-US16364.
XX
XX 22-MAY-2000; 2000US-0576424.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Hanna N, Brams P;
PI WPI; 2002-089895/12.
DR N-PSDB; AAS17246.
XX
XX Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, as
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy
XX
XX Example 8; Fig 5a; 89pp; English.
XX
XX The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present protein
CC sequence represents the light chain of 16C10, a primatized antibody
CC used in the invention to induce apoptosis and inhibit production of
CC interleukin-2 (IL-2).
XX
XX Sequence 236 AA;
SQ
Query Match 100.0%; Score 1232; DB 23; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e-66;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRVPAQLLGLLLLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIGGYDLHWYQQL 60
DB 1 MRVPAQLLGLLLLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIGGYDLHWYQQL 60
QY 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYOSYSSSLNAQV 120
DB 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYCYOSYSSSLNAQV 120
QY 121 FGGGTRTLVGLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FGGGTRTLVGLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 181 AGVETTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 AGVETTPSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
RESULT 3
AAU01821
ID AAU01821 standard; Protein; 236 AA.
XX AAU01821;
XX
XX 25-MAY-1997 (first entry)
XX
XX Primatized anti-human B7.1 antigen antibody 16C10 light chain.
DE

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 6.50958 Seconds
(without alignments)
1704.917 Million cell updates/sec

Title: US-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPAQLLGLLLWLPQARC.....CQVTHEGSIVKTVAPTECS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	44.5	105	1	LAC_HUMAN
2	527	42.8	213	1	LLC1_HUMAN
3	463	37.6	130	1	LV1G_HUMAN
4	454	36.9	111	1	LV1D_HUMAN
5	432	35.1	111	1	LV1C_HUMAN
6	426	34.6	109	1	LV1F_HUMAN
7	424.5	34.5	112	1	LV2K_HUMAN
8	415	33.7	105	1	LAC_PIG
9	413.5	33.6	112	1	LV1H_HUMAN
10	412	33.4	105	1	LAC1_MOUSE
11	407.5	33.1	112	1	LV1E_HUMAN
12	402	32.6	109	1	LV1I_HUMAN
13	399	32.4	105	1	LAC_RABIT
14	396	32.1	111	1	LV1A_HUMAN
15	396	32.1	111	1	LV2B_HUMAN
16	395	32.1	111	1	LV2H_HUMAN
17	393	31.9	103	1	LV1E_HUMAN
18	392	31.8	111	1	LV2F_HUMAN
19	391	31.7	111	1	LV2I_HUMAN
20	385.5	31.3	104	1	LAC1_RAT
21	381	30.9	111	1	LV2D_HUMAN
22	380.5	30.9	104	1	LAC2_RAT
23	377	30.6	105	1	LAC5_MOUSE
24	374.5	30.4	104	1	LAC3_MOUSE
25	372	30.2	111	1	LV2A_HUMAN
26	371	30.1	111	1	LV2C_HUMAN
27	370	30.0	109	1	LV2E_HUMAN
28	369.5	30.0	104	1	LAC2_MOUSE
29	368	29.9	111	1	LV2G_HUMAN
30	352.5	28.6	110	1	LV2J_HUMAN
31	347	28.2	105	1	LAC5_MOUSE
32	344.5	28.0	112	1	LV6A_HUMAN
33	342	27.8	111	1	LV6C_HUMAN

ALIGNMENTS				
RESULT 1				
ID	LAC_HUMAN	STANDARD;	PRT;	105 AA.
AC	P01842; P80423;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig lambda chain C regions.			
GN	IGLC1 AND IGLC2 AND IGLC3.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (BENCE-JONES PROTEIN SH).			
RX	MEDLINE=70166723; PubMed=4909564;			
RA	Titani K., Wikler M., Shinoda T., Putnam F.W.;			
RT	"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide bridges."			
RL	J. Biol. Chem. 245:2171-2176(1970).			
RN	[2]			
RP	SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.			
RX	MEDLINE=69088380; PubMed=4883841;			
RA	Milstein C., Clegg J.B., Jarvis J.M.;			
RT	"Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jones protein."			
RL	Biochem. J. 110:631-652(1968).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN NIG-64).			
RX	MEDLINE=83186114; PubMed=6404900;			
RA	Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T., Shimizu A.;			
RT	"Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subgroup."			
RL	J. Biochem. 93:421-429(1983).			
RN	[4]			
RP	SEQUENCE (BENCE-JONES PROTEIN KERN).			
RX	MEDLINE=71150336; PubMed=5549568;			
RA	Ponstingl H., Hess M., Hilschmann N.;			
RT	"Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein kern). V. The complete amino acid sequence and its genetic interpretation."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).			
RN	[5]			
RP	PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).			
RX	MEDLINE=74109253; PubMed=4814727;			
RA	Chen B.L., Poljak R.J.;			
RT	"Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin (IgG New)."			
RL	Biochemistry 13:1295-1302(1974).			
RN	[6]			
RP	SEQUENCE (DOT).			
RX	MEDLINE=95255298; PubMed=7737190;			
RA	Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;			

34	341	27.7	111	1	LV6D_HUMAN	P06318	homo sapien
35	340.5	27.6	129	1	KV1W_HUMAN	P04431	homo sapien
36	339	27.5	108	1	LV3A_HUMAN	P01714	homo sapien
37	339	27.5	111	1	LV3B_HUMAN	P80748	homo sapien
38	334.5	27.2	131	1	LV6E_HUMAN	P06319	homo sapien
39	329.5	26.7	117	1	KV1U_HUMAN	P01602	homo sapien
40	326.5	26.5	103	1	LAC_CHICK	P20763	gallus gall
41	326	26.5	106	1	LV4E_HUMAN	P06889	homo sapien
42	322	26.1	108	1	LV5A_HUMAN	P01719	homo sapien
43	319	25.9	106	1	LV4B_HUMAN	P01716	homo sapien
44	318	25.8	106	1	LV4A_HUMAN	P01715	homo sapien
45	314	25.5	111	1	LV2L_HUMAN	P80422	homo sapien

RT "Characterization of the two unique human anti-flavin monoclonal
 RL immunoglobulins".
 RN Eur. J. Biochem. 228:886-893(1995).
 RP [7]
 RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEMM.
 RA MEDLINE=75046825; PubMed=4215080;
 RA Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
 RA Saul F.;
 RT "The three-dimensional structure of the fab' fragment of a human
 RT myeloma immunoglobulin at 2.0-A resolution".
 RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
 RN [8]
 RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
 RX MEDLINE=75013804; PubMed=4415202;
 RA Fett J.W., Deutsch H.F.;
 RT "Primary structure of the Mcg lambda chain.";
 RL Biochemistry 13:4102-4114(1974).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
 RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
 RA Panagiotopoulos N.;
 RT "Rotational allomerism and divergent evolution of domains in
 RT immunoglobulin light chains.";
 RL Biochemistry 14:3953-3961(1975).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY OF MCG.
 RX MEDLINE=90133913; PubMed=2515285;
 RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
 RT "Three-dimensional structure of a light chain dimer crystallized in
 RT water. Conformational flexibility of a molecule in two crystal
 RT forms.";
 RL J. Mol. Biol. 210:601-615(1989).
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82080680; PubMed=6273747;
 RA Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
 RT "Clustered arrangement of immunoglobulin lambda constant region genes
 RT in man.";
 RL Nature 294:536-540(1981).
 CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
 CC FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE
 CC KERN+ MARKER, THE NEMM PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN
 CC HAS THE KERN+ MARKER, AND THE MCG+ MARKER.
 CC -!- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
 CC 3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE
 CC (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
 CC SEQUENCE (LAMBDA-3).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; J00253; AAA59107.1; .
 DR EMBL; L38562; AAB36581.1; ALT_INIT.
 DR EMBL; X51754; CAB38569.1; ALT_INIT.
 DR EMBL; X51755; CAA36049.1; .
 DR EMBL; X51755; CAA36051.1; .
 DR F01; A92057; L2HU.
 DR PDB; 2MCG; 15-JUL-92.
 DR PDB; 7FAB; 31-JAN-94.
 DR PDB; 1AQK; 04-FEB-98.
 DR PDB; 1LIL; 15-MAY-97.
 DR Genew; HGNC:5855; IGLC1.
 DR Genew; HGNC:5856; IGLC2.
 DR Genew; HGNC:5857; IGLC3.
 DR MIM; 147220; .
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00407; IGL1; 1.
 DR PROSITE: PS00835; IG-LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Bence-Jones protein;
 KW 3D-structure. 1 1
 FT NON_TER 6 100 IG-LIKE.
 FT DOMAIN 27 86
 FT DISULFID 104 104
 FT VARIANT 5 5
 FT VARIANT 7 7
 FT VARIANT 45 45
 FT VARIANT 56 56
 FT VARIANT 82 82
 FT STRAND 8 11
 FT HELIX 15 19
 FT TURN 20 21
 FT STRAND 24 32
 FT STRAND 38 43
 FT TURN 44 45
 FT STRAND 46 48
 FT STRAND 52 59
 FT TURN 61 62
 FT STRAND 65 72
 FT HELIX 75 80
 FT STRAND 84 89
 FT STRAND 94 99
 SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;
 Query Match 44.5%; Score 548; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-36; Mismatches 0; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSPVKAGVETTPSKQ 191
 Db 1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSPVKAGVETTPSKQ 60
 QY 192 SNKKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 236
 Db 61 SNKKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 105
 RESULT 2
 ID ILL1_HUMAN STANDARD; PRT; 213 AA.
 AC P15814; 1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
 DE related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
 DE (CD179b antigen).
 GN IGL1 OR IGL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89315835; PubMed=2501791;
 RA Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
 RA McKearn J.P.;
 RT "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
 RT expressed in pre-B cells and may encode the human immunoglobulin

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Run on: October 2, 2003, 08:56:23 ; Search time 22.8387 Seconds
(without alignments)
2666.544 Million cell updates

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Total number of hits,satisfying chosen parameters: 830525

Food & Drug Administration

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1: sp_archea:*
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5: sp_invertebrate:*

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9: sp_phage:*
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13: sp_vertebra
14: sp_uncl
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17: sp_cheap:
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score greater than or equal to 100 and is derived by analysis of variance.

Result	Query
--------	-------

1	1045	84.8	237	4
2	1045	84.8	237	4

6	888	72.1	233
6	888	72.1	233

10	722	58.6	235	11
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14	472	38.3	130	11
----	-----	------	-----	----

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	1045	84.8	237	4	O8WUK4	homo sapien
2	1045	84.8	237	4	O8WUT6	homo sapien
3	991.5	80.5	236	4	O96861	homo sapien
4	977.5	79.3	236	4	O8NEJ1	homo sapien
5	891	72.3	234	4	O8N355	homo sapien
6	888	72.1	233	4	O8TBC9	homo sapien
7	871	70.7	233	4	O8N5F4	homo sapien
8	805.5	65.4	233	4	O96169	homo sapien
9	767.5	62.3	240	4	O8WUK3	homo sapien
10	722	58.6	235	11	O95M11	mus musculus
11	551	44.7	106	4	O8TCT5	homo sapien
12	496.5	40.3	234	4	O8NEK1	homo sapien
13	488.5	39.7	234	11	O8VCP0	mus musculus
14	472	38.3	130	11	O9DBW4	mus musculus
15	472	38.3	239	4	O8TCD0	homo sapien
16	469	38.1	239	4	O8NEK0	homo sapien

ALIGNMENTS

Q8WUK4

AC Q8WUK4;

DE Hypothetical protein.

NCBI_TaxID=9606;

ISSUE-FOCUS:
RA
Strausberg R.;

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DR      IPR003596; Iq v.
DR      InterPro: IPR003596; Iq v.
DR      InCelPro; IPR003596; Iq_MHC.

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PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.

Query Match	84.8%	score 1045;	DE
Best Local Similarity	88.4%	pred No	2 2e-8

qy / LGLLLNLPGARCESVLTQPFSVSGAPQKVTS

66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQ

125 TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL

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Db 126 TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185
QY 185 TTTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
Db 186 TTTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 237

RESULT 2
Q8WTU6 PRELIMINARY; PRT; 237 AA.
AC Q8WTU6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022098; AAH22098.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;

Query Match 84.8%; Score 1045; DB 4; Length 237;
Best Local Similarity 88.4%; Pred. No. 2.2e-83;
Matches 205; Conservative 10; Mismatches 15; Indels 2; Gaps 2;

QY 7 LLGILLWLPGARCESVLTQPPSVGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
Db 6 LLTLTLLAHCTGSAQSVLTQPPSVGAPGQKVTISCTGSSSNICAGYDVHWYQQLPGTAP 65
QY 66 KLLIYDINKRPSGISDRFSGSKSGTAAASLAITGLQTEDEADYQCSDSSINAO-VFEGG 124
Db 66 KLLIYGNRPSGVPDRFSGSKSGTASLAITGLQAEDEADYQCSDYLSASGVFEGG 125
QY 125 TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
Db 126 TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185
QY 185 TTTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
Db 186 TTTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 237

RESULT 3
Q96E61 PRELIMINARY; PRT; 236 AA.
AC Q96E61;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 79.3%; Score 977.5; DB 4; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.7e-77;
Matches 189; Conservative 20; Mismatches 21; Indels 1; Gaps 1;
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RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 80.5%; Score 991.5; DB 4; Length 236;
Best Local Similarity 83.1%; Pred. No. 1e-78;
Matches 192; Conservative 12; Mismatches 26; Indels 1; Gaps 1;

QY 7 LLGILLWLPGARCESVLTQPPSVGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
Db 6 LLTLTLLAHCTGSAQSVLTQPPSVGAPGQKVTISCTGSTSNIGAGYAVHWYQQPPGAAP 65
QY 66 KLLIYDINKRPSGISDRFSGSKSGTAAASLAITGLQTEDEADYQCSDSSINAOVFEGGT 125
Db 66 KLLIYGNRPSGVPDRFSGSKSGTASLAITGLQAEDEADYQCSDYLSGSVFGAGT 125
QY 126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185
Db 126 KVTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVE 185
QY 186 TTTPSKQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236
Db 186 TRPSQSNKKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS 236

RESULT 4
Q8NEJ1 PRELIMINARY; PRT; 236 AA.
AC Q8NEJ1;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 79.3%; Score 977.5; DB 4; Length 236;
Best Local Similarity 81.8%; Pred. No. 1.7e-77;
Matches 189; Conservative 20; Mismatches 21; Indels 1; Gaps 1;
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QY 7 LLGILLWLPGARCESVLTQPPSVGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP 66
Db 6 LLTLTLLAHCTGSAQSVLTQPPSVGAPGQKVTISCSGRSNIGSNVYVWYQVQVFGTAPK 65
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 09:12:09 ; Search time 10.4815 Seconds
(without alignments)
952.662 Million cell updates/sec

Title: US-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPAQLGLLLWLPARGC.....CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1232	100.0	236	3	US-08-487-550-10
2	1232	100.0	236	4	US-08-526-098-10
3	1052.5	85.4	236	3	US-08-049-672A-7
4	979	79.5	234	4	US-08-372-425A-4
5	973	79.0	234	3	US-08-487-550-2
6	973	79.0	234	4	US-08-526-098-2
7	965	78.3	235	3	US-08-049-672A-10
8	965	78.3	235	3	US-08-049-672A-12
9	955	77.5	235	2	US-08-378-939-12
10	885	71.8	235	4	US-08-152-060-70
11	882	71.6	235	4	US-08-152-060-88
12	857.5	69.6	233	3	US-08-523-894-6
13	836	67.9	240	3	US-08-049-672A-11
14	804.5	65.3	238	4	US-08-793-450-5
15	634.5	51.5	229	3	US-08-751-359-22
16	634.5	51.5	229	4	US-08-907-146-22
17	567	46.0	109	2	US-08-761-277A-51
18	548	44.5	105	1	US-08-422-091-9
19	548	44.5	105	1	US-08-422-091-9
20	548	44.5	105	2	US-08-422-092-9
21	548	44.5	105	2	US-08-788-800-6
22	548	44.5	105	3	US-08-422-093-9
23	548	44.5	105	3	US-08-422-112-9
24	544.5	44.2	200	6	5189147-10
25	543	44.1	106	4	US-09-313-942-14
26	535	43.4	104	4	US-09-025-769B-170
27	522	42.4	241	2	US-07-916-098A-56

28 508.5 41.3 236 1 US-08-157-101A-5 Sequence 5, Appli
29 508 41.2 235 1 US-08-276-852-153 Sequence 153, App
30 508 41.2 235 1 US-08-899-575-153 Sequence 153, App
31 508 41.2 235 1 US-08-899-575-153 Sequence 153, App
32 508 41.2 235 5 PCT-US95-08743-153 Sequence 153, App
33 502.5 40.8 235 3 US-08-812-586-16 Sequence 16, Appl
34 502.5 40.8 235 4 US-09-535-832A-17 Sequence 17, Appl
35 499 40.5 234 4 US-09-740-002-26 Sequence 26, Appl
36 496.5 40.3 131 1 US-08-305-683A-4 Sequence 4, Appli
37 492.5 40.0 234 3 US-09-049-672A-6 Sequence 6, Appli
38 492.5 40.0 234 5 PCT-US94-07659-4 Sequence 4, Appli
39 492.5 40.0 310 4 US-09-079-029-11 Sequence 11, Appli
40 484.5 39.3 234 4 US-09-740-002-24 Sequence 24, Appl
41 483 39.2 242 4 US-09-479-614-20 Sequence 20, Appl
42 482.5 39.2 234 2 US-07-590-192-2 Sequence 2, Appli
43 476 38.6 112 4 US-09-825-769B-18 Sequence 18, Appl
44 475 38.6 239 1 US-08-353-400-37 Sequence 37, Appl
45 472 38.3 239 3 US-08-487-550-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-487-550-10
; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO. 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-10

Query Match 100.0%; Score 1232; DB 3; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.7e-91;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPARGCESVLTPPSVSGAPQKVTISCTGSTSNIGGYDLHWYQOL 60
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Db 1 MRVPAQLGLLLWLPARGCESVLTPPSVSGAPQKVTISCTGSTSNIGGYDLHWYQOL 60
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QY 61 PGTAPELLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYQCQSDSLNAQV 120
DB 61 PGTAPELLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYQCQSDSLNAQV 120
QY 121 FGGGRLTLVLOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FGGGRLTLVLOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 181 AGVETTPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 AGVETTPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 2
US-09-526-098-10
; Sequence 10, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dartell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526.098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-10

Query Match 100.0%; Score 1232; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.7e-91;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPARGCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
DB 1 MRVPAQLGLLLWLPARGCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
QY 61 PGTAPELLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYQCQSDSLNAQV 120
DB 61 PGTAPELLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYQCQSDSLNAQV 120
QY 121 FGGGRLTLVLOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

DB 121 FGGGRLTLVLOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 181 AGVETTPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 AGVETTPSKSNKNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 3
US-09-049-672A-7
; Sequence 7, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lai, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 556
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ADRETUT05
; CLONE: 2492122
US-09-049-672A-7

Query Match 85.4%; Score 1052.5; DB 3; Length 236;
Best Local Similarity 88.3%; Pred. No. 4.2e-77;
Matches 204; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 7 LLGALLLWLPARGCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
DB 6 LLLTLLACTGSAQSVLTQPPSVSGAPGQKVTISCTGSSNIGAGYDVHWIQLPGTAP 65
QY 66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYQCQSDSLNAQVFGGGT 125
DB 66 KLLIYGSNRPSGVPDRFSGSKSGTASLAITGLQAEADYQCQSDSLSGVVFGGGT 125

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 09:18:44 ; Search time 88.5965 Seconds
(without alignments)
421.442 Million cell updates/sec

Title: US-09-758-173-10

Perfect score: 1232

Sequence: 1 MRVPAQLGLLLWLPGAR.....CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1232	100.0	236	10	US-09-948-429B-10
2	1232	100.0	236	12	US-10-124-807-10
3	1232	100.0	236	12	US-10-291-532-10
4	1232	100.0	236	14	US-10-124-905-10
5	1006	81.7	235	10	US-09-747-669-6
6	1006	81.7	235	15	US-10-290-703-6
7	999.5	81.1	221	14	US-10-001-857-202
8	974	79.1	234	12	US-10-194-801C-4
9	973	79.0	234	10	US-09-948-429B-2
10	973	79.0	234	12	US-10-124-807-2
11	973	79.0	234	12	US-10-291-532-2
12	973	79.0	234	14	US-10-124-905-2
13	969	78.2	242	12	US-10-225-108A-14
14	950.5	77.2	219	10	US-09-974-449-38
15	916.5	74.4	219	15	US-10-026-925-57

16	910	73.9	214	11	US-09-972-656-96
17	909	73.8	218	11	US-09-972-656-102
18	907.5	73.7	217	11	US-09-972-656-88
19	897	72.8	216	11	US-09-972-656-90
20	888	72.1	218	11	US-09-791-153A-51
21	886	71.9	216	11	US-09-972-656-108
22	885	71.8	235	9	US-09-853-161-70
23	885	71.8	235	9	US-09-852-659A-70
24	885	71.8	235	10	US-09-852-797-70
25	882	71.6	235	9	US-09-853-161-88
26	882	71.6	235	9	US-09-852-659A-88
27	882	71.6	235	10	US-09-852-797-88
28	876.5	71.1	235	12	US-10-076-747-82
29	868	70.5	232	12	US-10-225-108A-12
30	860.5	69.8	229	12	US-10-310-719-36
31	857.5	69.6	233	15	US-10-211-357-6
32	854.5	69.4	244	9	US-09-925-301-1424
33	841	68.3	212	11	US-09-972-656-98
34	826	67.0	239	10	US-09-828-995B-26
35	816.5	66.3	239	15	US-10-221-945-2
36	815	66.2	216	10	US-09-736-371B-19
37	762.5	61.9	246	11	US-09-909-567B-49
38	683.5	55.5	216	9	US-09-291-299A-8
39	673	54.6	217	9	US-09-291-299A-7
40	639.5	51.9	216	9	US-09-291-299A-9
41	635.5	51.6	216	9	US-09-291-299A-10
42	569.5	46.2	147	11	US-09-988-115A-57
43	567	46.0	109	10	US-09-925-664-51
44	562	45.6	139	10	US-09-798-692-901
45	562	45.6	139	15	US-10-040-862-901

ALIGNMENTS

RESULT 1
US-09-948-429B-10
Sequence 10, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/948.429B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383.916

FILING DATE: US 08/487.550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

```

; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-10

Query Match          100.0%; Score 1232; DB 10; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.6e-90;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQOL 60
DB 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQOL 60
QY 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYICQSYDSSLSNAQV 120
DB 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQOL 60
QY 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYICQSYDSSLSNAQV 120
DB 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYICQSYDSSLSNAQV 120
QY 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 181 AGVETTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 AGVETTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 2
US-10-124-807-10
; Sequence 10, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; ATTORNEY/AGENT INFORMATION:
; NAME: teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-10-124-807-10

Query Match          100.0%; Score 1232; DB 12; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.6e-90;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQOL 60
DB 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQOL 60
QY 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYICQSYDSSLSNAQV 120
DB 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYICQSYDSSLSNAQV 120
QY 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
QY 181 AGVETTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
DB 181 AGVETTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 3
US-10-291-532-10
; Sequence 10, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/383,916
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 08/487,950
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primatized peptide sequence
US-10-291-532-10

Query Match          100.0%; Score 1232; DB 12; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.6e-90;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQOL 60
DB 1 MRVPAQLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQOL 60
QY 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYICQSYDSSLSNAQV 120
DB 61 PGTAPKLLIYDINKRPSGISDRFSGSKGTAASLAITGLQTEDEADYICQSYDSSLSNAQV 120
QY 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
DB 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 ; Search time 3758.85 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-11

Perfect score: 1431

Sequence: 1 ATGAACACCTGTGTTCTT.....CCCTGTCTCCGGTAATGA 1431

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
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28: em.un.*
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30: em.htg.hum.*
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41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1431	100.0	1431	6	AR108867 Sequence
2	1431	100.0	1431	6	AR265201 Sequence
3	1429.4	99.9	1431	6	BD063039 Identific
4	1315.8	91.9	1431	6	AR108863 Sequence
5	1315.8	91.9	1431	6	AR285197 Sequence
6	1314.2	91.8	1431	6	BD063035 Identific
7	1276.4	89.2	1567	6	AR135359 Sequence
8	1261.2	88.1	1431	6	E10697
9	1256.8	87.8	1594	9	AK057754 Homo sapi
10	1251.6	87.5	1596	9	AK098516 Homo sapi
11	1236.8	86.4	1589	9	AK057775 Homo sapi
12	1234.8	85.6	1418	6	A49389 Sequence 7
13	1213.6	84.8	1418	6	AR176296 Sequence
14	1192.8	82.7	1566	9	AK097365 Homo sapi
15	1181	82.5	1404	6	AR135375 Sequence
16	1177.8	82.2	1404	6	AR135377 Sequence
17	1176.2	82.2	1404	6	AR135376 Sequence
18	1151	80.4	1428	6	BD097232 A therape
19	1142.6	79.8	1630	9	BC024289 Homo sapi
20	1134.8	79.3	1428	6	AR031184 Sequence
21	1134.8	79.3	1428	6	AR042589 Sequence
22	1134.8	79.3	1428	6	AR059282 Sequence
23	1134.8	79.3	1428	6	AR076260 Sequence
24	1134.8	79.3	1428	6	AR300617 Sequence
25	1134	79.2	1425	9	AY172959 Homo sapi
26	1134	79.2	1430	6	AX419496 Sequence
27	1134	79.2	1673	9	HS1GGL1H
28	1133.8	79.2	1507	6	BD000501 Process f
29	1131.8	79.1	1679	9	BC018747 Homo sapi
30	1130.6	79.0	1633	9	AK097859 Homo sapi
31	1125.2	78.6	1428	6	AR031186 Sequence
32	1125.2	78.6	1428	6	AR042591 Sequence
33	1125.2	78.6	1428	6	AR059284 Sequence
34	1125.2	78.6	1428	6	AR076262 Sequence
35	1125.2	78.6	1428	6	AR300619 Sequence
36	1122.8	78.5	1599	6	AX330501 Sequence
37	1122.8	78.5	1599	6	AX333307 Sequence
38	1122.8	78.5	1599	6	AX334122 Sequence
39	1122.8	78.5	1599	6	HUMIGHEPAH
40	1122.8	78.5	3143	9	BC019046 Homo sapi
41	1122	78.4	1990	9	AK098817 Homo sapi
42	1121.2	78.4	1549	6	A21385 Plasmid DNA
43	1121.2	78.4	1617	6	A29585 H.sapiens c
44	1118	78.1	1431	9	AY172957 Homo sapi
45	1118	78.1	1449	6	BD078407 Antigen-b

ALIGNMENTS

RESULT 1
AR108867
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR108867
Sequence 11 from patent US 6113898.
AR108867
Sequence 11 from patent US 6113898.
AR108867.1 GI:12825143
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1431)
Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
Patent: US 6113898-A 11 05-SEP-2000;
linear PAT 14-FEB-2001

Pred. No. is the number of results predicted by chance to have a

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 12:12:30 ; Search time 293.094 Seconds
(without alignments)
13179.730 Million cell updates/sec

Title: US-09-758-173-11
Perfect score: 1431
Sequence: 1 ATGAACACCTGCTGCTTT.....CCCTGCTCGGGTAAATGA 1431

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	18	Primate anti-hu
2	1431	100.0	1431	19	Macaque primatized
3	1431	100.0	1431	24	DNA sequence of a
4	1315.8	91.9	1431	18	Primate anti-hu
5	1315.8	91.9	1431	19	Macaque primatized
6	1315.8	91.9	1431	24	DNA sequence of a
7	1276.4	89.2	1567	22	Human immune syste
8	1261.2	88.1	1431	17	Monoclonal antibod

9	1261	88.1	1634	21	AAZ50012	Human immune syste
10	1224.8	85.6	1418	17	AAT62889	Anti-rhesus D reco
11	1181	82.5	1404	18	AAT62868	Human gamma-4 heav
12	1177.8	82.3	1404	18	AAT62870	Human gamma-4E he
13	1176.2	82.2	1404	18	AAT62869	Human gamma-4E hea
14	1151	80.4	1428	22	AAH7480	Nucleotide sequenc
15	1151	80.4	1428	25	ABT34317	Hepatitis C virus
16	1136.4	79.4	1428	18	AAT61241	Human anti-RSV mon
17	1134	79.2	1430	24	AAK98701	CDNA of the heavy
18	1134	79.2	1430	25	ABX12855	Human monoclonal r
19	1134	79.2	1644	22	AAS22593	Human cDNA encodin
20	1133.8	79.2	1507	21	AAA09695	Human immunoglobul
21	1133.4	79.2	1798	21	AAC98220	Human colon cancer
22	1123.6	78.5	1428	18	AAT61279	Human anti-RSV mon
23	1122.8	78.5	1599	24	ABK64550	Human benign prost
24	1122.8	78.5	1599	24	ABL65479	Colon adenocarcino
25	1122.8	78.5	1599	24	ABL65479	Lung cancer relate
26	1122.8	78.5	1599	24	ABL65479	Lung cancer relate
27	1121.2	78.4	1617	14	AAQ35099	Antibody D heavy c
28	1120.8	78.3	19035	19	AAQ61794	Traget plasmid Man
29	1119.6	78.2	1549	13	AAQ20066	Encodes heavy chai
30	1119	78.2	1442	22	AAQ84208	Plasmid Glambda-1B
31	1118	78.1	1449	20	AAQ84208	Monoclonal antibod
32	1118	78.1	1449	20	AAQ84208	Monoclonal antibod
33	1115.8	78.0	6281	22	AAQ84206	Plasmid Glambda-1A
34	1112.4	77.7	1437	19	AAV35487	Macaque primatized
35	1112.4	77.7	1437	24	AAV17245	DNA sequence of a
36	1110.8	77.6	1427	19	AAV14429	Plasmid Hu19HCPcd
37	1110.8	77.6	1427	19	AAV14431	Plasmid Hu19HCPcd
38	1110.8	77.6	1427	18	AAV13847	Primate anti-hu
39	1109.8	77.6	1458	13	AAQ23571	Reshaped CD4 antib
40	1109.8	77.5	1458	13	AAQ23581	Reshaped CD4 antib
41	1109.2	77.5	1427	19	AAV41432	Plasmid Hu19HCPcd
42	1107.8	77.4	1576	14	AAQ49944	Human anti-HBs hea
43	1107.4	77.4	1416	25	AB224539	Humanized 10D5 ant
44	1104.8	77.2	1392	25	ABD53212	BIWA4/8 antibody h
45	1104.8	77.2	9568	25	ABD53219	BIWA4 antibody DNA

ALIGNMENTS

RESULT 1
AAT62513
ID AAT62513 standard; DNA; 1431 BP.
XX
AC AAT62513;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primatized anti-human B7.1 antigen antibody 16C10 heavy chain DNA.

XX Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW Primatized antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brans P, Hanna N, Shestowsky WS;

XX		WFI; 1997-108638/10.
DR		P-FSDB; AAW01822.
DR		
XX		Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT		useful for treating autoimmune disease or graft-versus-host disease
XX		
PS	Claim 11; Fig 10B; 81pp; English.	
XX		
CC	2 DNA sequences (AAW62512 and AAW62513) respectively code for	
CC	primatised forms (AAW01821 and AAW01822) of the light and heavy chains	
CC	of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody	
CC	16C10. Cloned 16C10 light and heavy variable genes are inserted	
CC	into an expression vector (pref. NEOSPLA) which contains human light	
CC	and heavy chain constant region genes to allow prodn. of primatised	
CC	antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1	
CC	antibodies have also been produced (see also AAW01817-20). The	
CC	primatised antibodies inhibit the B7:CD28 pathway, making them	
CC	useful immunosuppressants for the treatment of autoimmune disorders	
CC	and graft-versus-host disease.	
XX		
SQ	Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;	
	Query Match	100.0%; Score 1431; DB 18; Length 1431;
	Best Local Similarity	100.0%; Pred.No 6.3e+286;
	Matches 1431; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Dd	1	ATGAACACCTGTGGTTCTTCTCCTCCTGCTGGTGCGAGCTCCCAGATGGGTGTGCCAG 60
QY	61	GTCGAGCTGCAGGAGTGGGGCCAGGACTGTTGAAGCTTCGGAGAGCCCTGTCCTCAC 120
Dd	61	GTCGAGCTGCAGGAGTGGGGCCAGGACTGTTGAAGCTTCGGAGAGCCCTGTCCTCAC 120
QY	121	TGCGTGTCTCTGPHGGTCCATCAGCGGTGGTTATGGCTGGGGCTGGATTCGCCAGGCC 180
Dd	121	TGCGTGTCTCTGPHGGTCCATCAGCGGTGGTTATGGCTGGGGCTGGATTCGCCAGGCC 180
QY	181	CCAGGGAAGGGGCTGGAGTGGATTGGAGTTCTCATAGTAGTAGTGGGAACACCTACTAC 240
Dd	181	CCAGGGAAGGGGCTGGAGTGGATTGGAGTTCTCATAGTAGTAGTGGGAACACCTACTAC 240
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Dd	241	RACCCCTCCCTCAAGAGTCAAGTACCATTTCACACACAGCTCCAAGAACCAAGTCTCC 300
QY	301	CTGAAGCTGAACCTCTATGACCGCCGCGACACGGCCGCTGATTACTGTGTGAGAGATCGT 360
Dd	301	CTGAAGCTGAACCTCTATGACCGCCGCGACACGGCCGCTGATTACTGTGTGAGAGATCGT 360
QY	361	CNTTTTTCAAGTTGTGGAATGGTTTACAACACTGGTTTCATGTCTGGGGCCGGGAGTCC 420
Dd	361	CNTTTTTCAAGTTGTGGAATGGTTTACAACACTGGTTTCATGTCTGGGGCCGGGAGTCC 420
QY	421	CTGGTCAACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGCTCTTCCCCCTGGCACCCCTCC 480
Dd	421	CTGGTCAACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGCTCTTCCCCCTGGCACCCCTCC 480
QY	481	TCCAGAGCACCTCTTGGGGGACAGCGGCCCTGGGCTGCCCTGTCAAGACTACTTCCCC 540
Dd	481	TCCAGAGCACCTCTTGGGGGACAGCGGCCCTGGGCTGCCCTGTCAAGACTACTTCCCC 540
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Dd	541	GAACCGGTGACGGTGTCTGTGGAATCTGAGCGGCCCTGACACAGCGCGCTGACACCTTCCCG 600
QY	601	GCTGTCCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGTACCGTGCCTCCAGC 660
Dd	601	GCTGTCCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGTACCGTGCCTCCAGC 660
QY	661	AGCTTGGGCACCCAGCACCTACTCTGCAAGCTGAATCACAAGGCCCGACACCAAGGTG 720

Db	661	AGTTGGGACCAGACCTACATCTGCAACGTTGAATCACAAAGCCGACACAAACCAAGGTG	720
QY	721	GACAAGAAAGCAGAGCCCAAATCTGTGACAAAACTCACACATGCCACACGTTGCCACGCA	780
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QY	901	GAGGTCAAGTTCAACTGGTGGAGCGGTGAGTGCATATGTCATGATGTCACAAAGCCG	960
Db	901	GAGGTCAAGTTCAACTGGTGGAGCGGTGAGTGCATATGTCATGATGTCACAAAGCCG	960
QY	961	CGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCTGCTCACCGTCTTCCAGCC	1020
Db	961	CGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCTGCTCACCGTCTTCCAGCC	1020
QY	1021	GACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAAGAGCCCTCCAGACCC	1080
Db	1021	GACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAAGAGCCCTCCAGACCC	1080
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QY	1381	CTGCACAACCACTACAGCGAGAAGAGCCTCCCTGTCTCCGGGTAAATGA	1431
Db	1381	CTGCACAACCACTACAGCGAGAAGAGCCTCCCTGTCTCCGGGTAAATGA	1431
RESULT 2			
AAV35489			
ID	AAV35489 standard; DNA; 1431 BP.		
XX	AAV35489;		
XX	25-SEP-1998 (first entry)		
DT	Macaque primatized 16C10 heavy chain DNA.		
XX	Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;		
KW	CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;		
KW	T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;		
KW	immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;		
XX	T cell proliferation; ss.		
OS	Macaca fascicularis.		
XX	Key		
FH	Location/Qualifiers		
CD	1..1431		
FT	/*tag= a		
FT	/product= 16C10 heavy chain		
FT	FT		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:05:20 ; Search time 2366.54 Seconds
(without alignments)
14696.420 Million cell updates/sec

Title: US-09-758-173-11
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 22781392 seqs, 1215238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: em_estba:**
- 2: em_esthum:**
- 3: em_estin:**
- 4: em_estnu:**
- 5: em_estov:**
- 6: em_estpl:**
- 7: em_estro:**
- 8: em_hic:**
- 9: gb_est1:**
- 10: gb_est2:**
- 11: gb_hic:**
- 12: gb_est3:**
- 13: gb_est4:**
- 14: gb_est5:**
- 15: em_estfun:**
- 16: em_estom:**
- 17: em_gss_hum:**
- 18: em_gss_inv:**
- 19: em_gss_pln:**
- 20: em_gss_vrt:**
- 21: em_gss_fun:**
- 22: em_gss_mam:**
- 23: em_gss_mus:**
- 24: em_gss_pro:**
- 25: em_gss_rod:**
- 26: em_gss_pbg:**
- 27: em_gss_vrl:**
- 28: gb_gss1:**
- 29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	929.6	65.0	1142	13	BX414495 BX414495
c 3	902	63.0	1020	12	BQ062878 AGENCOURT
c 4	899.2	62.8	1045	13	BX337477 BX337477

c 5	894.8	62.5	1149	13	BX381020
c 6	892.6	62.4	1201	13	BX377803
c 7	891.2	62.3	1201	13	BX43438
c 8	889.8	62.2	902	13	BUI45962
c 9	875.8	61.2	1013	13	BX360518
c 10	867.6	60.6	1200	13	BX415883
c 11	864	60.4	947	13	BQ709771
c 12	850.4	59.4	958	13	BQ706140
c 13	849.2	59.3	1093	13	BX428863
c 14	842.4	58.9	926	10	BG755166
c 15	835.2	58.4	1096	13	BX415920
c 16	832	58.1	988	13	BQ708857
c 17	831.8	58.1	1201	13	BX338493
c 18	831.2	58.1	901	12	BM007892
c 19	830.6	58.0	985	13	BX457369
c 20	829.4	58.0	1201	13	BX417147
c 21	824.4	57.6	1029	12	BQ063185
c 22	823.2	57.5	1019	13	BX325650
c 23	822.8	57.5	887	13	BQ711255
c 24	822.2	57.5	918	13	BQ708022
c 25	818.6	57.2	995	12	BM914540
c 26	818	57.2	1015	13	BX367600
c 27	817.8	57.1	980	13	BX325701
c 28	811.8	56.7	889	13	BX346909
c 29	811	56.7	1147	13	BX360330
c 30	809	56.5	1009	13	BX456658
c 31	808.8	56.5	881	13	BQ711291
c 32	807.4	56.4	1200	13	BX456326
c 33	804	56.2	853	13	BX388631
c 34	801.6	56.0	862	13	BX450248
c 35	800.2	55.9	1031	13	BQ064886
c 36	799.4	55.9	852	13	BX450232
c 37	798.4	55.8	1004	13	BX432300
c 38	797.4	55.7	936	13	BQ711727
c 39	796	55.6	940	13	BQ705928
c 40	795.6	55.6	1070	13	BX397632
c 41	795.2	55.6	1152	13	BX339318
c 42	794.8	55.5	1201	13	BX380759
c 43	794.2	55.5	1151	13	BX378450
c 44	792.2	55.4	885	13	BX408117
c 45	791.2	55.3	1201	13	BX396322

ALIGNMENTS

RESULT 1
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DEFINITION clone CSODI009YJ10 3-PRIME, mRNA sequence.
ACCESSION BX377695
VERSION BX377695.1 GI:30439018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI009DE05NPI&cluster=7198.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600


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FEATURES
source
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/Note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Best Local Similarity 95.8%; Pred. No. 4e-215;
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RESULT 2
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LOCUS
DEFINITION
3-PRIME, mRNA sequence.
ACCESSION
BX414495
VERSION
BX414495.1 GI:30637021
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EST.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 1142)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
CONTACT
Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0CAP001AE07NP1&cluster=7198.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP001AE07NP1.
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1. 1142
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/Note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT
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Matches 952; Conservative 6; Mismatches 9; Indels 2; Gaps 2;
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DB 1078 TTCCTCCCTGGACCCCTCTCTCCAGAGCAGCTCTGGGGG-AMAGCGCCCTGGGCTGCTG 1020
QY 523 GTCAAGGAGTACTTCCCCCAAGCCCGTGTGAGGTGTGCTGGAACCTCAGGCGCCCTGACCA 582
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:10:05 ; Search time 76.0531 Seconds
(without alignments)
8304.972 Million cell updates/sec

Title: US-09-758-173-11
Perfect score: 1431
Sequence: 1 ATGAACACCGTGGTCTT.....CCCTGTCTCGGTAATGA 1431

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1276.4	89.2	1567	3	US-09-049-672A-17
6	1213.6	84.8	1416	4	US-08-793-450-7
7	1181	82.5	1404	3	US-08-523-894-7
8	1177.8	82.3	1404	3	US-08-523-894-11
9	1176.2	82.2	1404	3	US-08-523-894-9
10	1134.8	79.3	1428	1	US-08-488-376-17
11	1134.8	79.3	1428	2	US-08-634-223-17
12	1134.8	79.3	1428	2	US-08-634-224-17
13	1134.8	79.3	1428	2	US-08-634-400-17
14	1134.8	79.3	1428	2	US-08-635-878-17
15	1134.8	79.3	1428	2	US-08-770-057-17
16	1134.8	79.3	1428	3	US-09-335-697B-17
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32	1107.8	77.4	1576	1	US-08-157-101A-6	Sequence 6, Appli
33	1102.2	77.0	6557	1	US-08-486-740-3	Sequence 3, Appli
34	1102.2	77.0	6557	5	PCT-US95-09576-3	Sequence 3, Appli
35	1097.8	76.7	1350	1	US-08-157-101A-9	Sequence 9, Appli
36	1096.6	76.6	9209	1	US-08-149-099C-3	Sequence 3, Appli
37	1096.6	76.6	9209	1	US-08-476-275-2	Sequence 2, Appli
38	1096.6	76.6	9209	2	US-08-478-967A-3	Sequence 3, Appli
39	1096.6	76.6	9209	4	US-08-475-815B-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
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: Sequence 11, Application US/08487550
: Patent No. 6113698
: GENERAL INFORMATION:
: APPLICANT: Anderson, Darrell R.
: TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
: IMMUNOSUPPRESSANTS"
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,550
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Teskin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-131
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1431 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1431
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 1..1431
US-08-487-550-11

Query Match 100.0%; Score 1431; DB 3; Length 1431;

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.
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 (without alignments)
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Title: US-09-758-173-11
 Perfect score: 1431
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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues
 Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_NA:*

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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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3	1431	100.0	1431 12	US-10-291-532-11	Sequence 11, Appl
4	1431	100.0	1431 13	US-10-124-905-11	Sequence 11, Appl
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6	1315.8	91.9	1431 10	US-09-948-429B-3	Sequence 3, Appl
7	1315.8	91.9	1431 12	US-10-124-807-3	Sequence 3, Appl
8	1315.8	91.9	1431 12	US-10-291-532-3	Sequence 3, Appl
9	1315.8	91.9	1431 13	US-10-124-905-3	Sequence 3, Appl
10	1314.2	91.8	1431 13	US-10-073-138-2	Sequence 3, Appl
11	1118.1	82.5	1404 14	US-10-211-357-7	Sequence 2, Appl
12	1177.8	82.3	1404 14	US-10-211-357-11	Sequence 2, Appl
13	1176.2	82.2	1404 14	US-10-211-357-9	Sequence 11, Appl
14	1151.8	80.4	1428 12	US-10-203-754A-40	Sequence 9, Appl
15	1134.8	79.3	1428 9	US-09-740-002-17	Sequence 40, Appl
16	1134	79.2	1430 12	US-10-225-108A-1	Sequence 17, Appl
					Sequence 1, Appl

17	1134	79.2	1430	12	US-09-848-832-1	Sequence 1, Appl
18	1133.4	79.2	1798	9	US-09-925-299-230	Sequence 230, App
19	1133.4	79.2	1798	11	US-09-925-299-230	Sequence 230, App
20	1125.2	78.6	1428	9	US-09-740-002-19	Sequence 19, Appl
21	1122.8	78.5	1599	10	US-09-954-456-789	Sequence 789, App
22	1122.8	78.5	1599	10	US-09-954-456-789	Sequence 789, App
23	1122.8	78.5	1599	12	US-09-873-319-445	Sequence 1604, App
24	1122.8	78.5	1599	12	US-09-873-319-445	Sequence 445, App
25	1122.8	78.5	1599	12	US-09-960-706-704	Sequence 704, App
26	1118	78.1	1431	12	US-09-873-367C-1010	Sequence 1010, App
27	1118	78.1	1449	10	US-10-225-108A-15	Sequence 15, Appl
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36	1110.8	77.6	1427	13	US-10-073-138-4	Sequence 4, Appl
37	1110.8	77.6	1427	13	US-10-066-895-20	Sequence 20, Appl
38	1109.2	77.5	1427	13	US-10-066-895-25	Sequence 25, Appl
39	1104.8	77.2	1392	14	US-10-066-895-27	Sequence 27, Appl
40	1102.8	77.1	6284	13	US-10-150-475A-7	Sequence 7, Appl
41	1100.4	76.9	1356	10	US-10-066-895-14	Sequence 14, Appl
42	1100	76.9	1539	9	US-09-822-698A-27	Sequence 27, Appl
43	1098.2	76.7	1617	10	US-09-822-698A-87	Sequence 87, Appl
44	1096.6	76.6	9199	10	US-09-822-830A-571	Sequence 571, App
45	1096.6	76.6	9209	11	US-09-911-692-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1
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 ; Sequence 11, Application US/09948429B
 ; Patent No. US20020177689A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Darrell R.
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 ; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 ; IMMUNOSUPPRESSANTS"
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/948,429B
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/383,916
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/487,550
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-131
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021

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QY	181	CCAGGGAAGGGCTGGAGTGGATTGGAGTTCTATAGTAGTAGTGGGAACACCTACTAC	240	
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QY	781	CCTGAATCTCTGGGGGACCGTCTTCCTCTTCCCTCCCAACCAAGGACACCTCC	840	

GenCore version 5.1.6
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Title: US-09-758-173-12

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2342.5	91.9	473	22 AAB36206	Human immune syste
5	2309	90.6	476	18 AAW01818	Primates anti-hu
6	2309	90.6	476	19 AAW63761	Macaque primatized
7	2309	90.6	476	23 AAU11539	Protein sequence o
8	2296.5	90.1	475	17 AAR93553	Monoclonal antibody
9	2278	89.4	470	21 AAY44721	Human immune syste

10	2217	87.0	472	17	AA93166	Anti-rhesus D reco
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14	2148	84.3	470	13	AA922757	Reshaped CAMPARH-1
15	2145.5	84.2	467	18	AAW14927	Human gamma-4PE he
16	2144.5	84.1	467	18	AAW14925	Human gamma-4PE he
17	2138.5	83.9	446	17	AAW05829	Human gamma-4E ant
18	2137.5	83.9	467	18	AAW14926	Human gamma-4E ant
19	2134.5	83.7	581	22	AA811972	Ganglioside GD2 sp
20	2126.5	83.4	475	18	AAW11639	Human anti-RSV mon
21	2126.5	83.4	475	22	AA963640	Amino acid sequenc
22	2126	83.4	451	20	AAW50031	Human E27 anti-IGE
23	2126	83.4	451	20	AAW50031	Mus musculus anti-
24	2126	83.4	451	21	AAW07473	Amino acid sequenc
25	2126	83.4	451	22	AAW74212	E27 anti-IGE antib
26	2126	83.4	451	22	AAW76952	Full length heavy
27	2124	83.3	451	20	AAW95659	Mus musculus anti-
28	2124	83.3	451	20	AAW95661	Mus musculus anti-
29	2124	83.3	451	21	AAW85201	Light chain amino
30	2124	83.3	451	22	AAW47088	Anti-IGE antibody,
31	2124	83.3	451	22	AAW76948	Full length heavy
32	2124	83.3	451	22	AAW76950	Full length heavy
33	2122.5	83.3	450	22	AAE10515	Humanised high pot
34	2122.5	83.3	450	23	ABP66572	Humanised high pot
35	2122.5	83.3	450	23	ABP66572	Human RSV antibody
36	2122.5	83.3	450	24	ABU69435	Human RSV antibody
37	2122.5	83.3	450	24	ABU69467	Respiratory syncyt
38	2121	83.2	462	21	AAE26884	Respiratory syncyt
39	2120.5	83.2	450	22	AAE10521	Human immunoglobul
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41	2120.5	83.2	450	24	ABU69433	Human RSV antibody
42	2120.5	83.2	472	24	ABP58289	Respiratory syncyt
43	2119.5	83.2	450	22	AAE10511	Humanised 10D5 ant
44	2119.5	83.2	450	22	AAE10513	Humanised high pot
45	2119.5	83.2	450	23	ABP66576	Humanised high pot

ALIGNMENTS

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AC AAW01822;
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DT 25-MAY-1997 (first entry)
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DE Primatized anti-human B7.1 antigen antibody 16C10 heavy chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW primatized antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
FN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brans P, Hanna N, Shestowsky WS;
XX

DR WPI; 1997-108638/10.
 DR N-PSDB; AA62513.
 XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen
 PT useful for treating autoimmune disease or graft-versus-host disease
 XX
 PS Claim 14; Fig 10B; 81pp; English.
 XX
 CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
 CC heavy variable genes (see also AA62512 and AA62513) are inserted into
 CC an expression vector (pref. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
 CC antibodies have also been produced (see also AAW01817-20). The
 CC primatised antibodies inhibit the B7:CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.
 XX
 SQ Sequence 476 AA;
 Query Match 100.0%; Score 2549; DB 18; Length 476;
 Best Local Similarity 100.0%; Pred. No. 5.8e-149;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 181 EPVTSMNSGALTSQVHTFPVAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKSNTKV 240
 QY 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTEPYTCVVVDVSHEDP 300
 DB 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTEPYTCVVVDVSHEDP 300
 QY 301 EVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
 DB 301 EVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
 QY 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 DB 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTOKSLSPGK 476
 DB 421 KTTTPVLSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTOKSLSPGK 476

RESULT 2
 AAW63765
 ID AAW63765 standard; Protein; 476 AA.
 XX
 AC AAW63765;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primatised 16C10 heavy chain protein.
 XX
 KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;

KW T cell proliferation.
 XX
 OS Macaca fascicularis.
 XX
 PN WO9819706-A1.
 XX
 PD 14-MAY-1998.
 XX
 XX 29-OCT-1997; 97WO-US19906.
 PF
 XX 08-NOV-1996; 96US-0746361.
 PR
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX Anderson DR, Brams P, Hanna N;
 PI
 XX WPI; 1998-286601/25.
 DR
 DR N-PSDB; AAV35489.
 XX
 PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 PS
 XX Example 7; Fig 5b; 87pp; English.
 XX

This sequence represents a primatised form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs. CC host diseases, B cell lymphoma, infections (including by human immune CC deficiency virus) or inflammatory disease and tumours. Optionally the CC Mab can be conjugated to a drug or toxin, Mab's or their fragments, can CC also be used as imaging agents and as vaccines or immunogens to develop CC anti-idiotypic reagents. Mab's are optionally combined with other proteins CC or small molecule immunosuppressants. Blocking B7/CD28 interactions CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits CC production of interleukin-2 (IL-2), T cell proliferation and CC antigen-specific immunoglobulin G (IgG) responses.

SQ Sequence 476 AA;
 Query Match 100.0%; Score 2549; DB 19; Length 476;
 Best Local Similarity 100.0%; Pred. No. 5.8e-149;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSISSGGYGRWIRQP 60
 DB 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSISSGGYGRWIRQP 60
 QY 61 PKGLEWIGSFYSSSGNTYYNPSLKSOVTISTDTSKNQFSLKLSMTAAADTAVYVCVDR 120
 DB 61 PKGLEWIGSFYSSSGNTYYNPSLKSOVTISTDTSKNQFSLKLSMTAAADTAVYVCVDR 120
 QY 121 LFSVGVNMYNNWDFVWVGPGVLTVSSASTKGPSVFPLAPSSKTSSTGTAALCLVKDYFP 180
 DB 121 LFSVGVNMYNNWDFVWVGPGVLTVSSASTKGPSVFPLAPSSKTSSTGTAALCLVKDYFP 180
 QY 181 EPVTSMNSGALTSQVHTFPVAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKSNTKV 240
 DB 181 EPVTSMNSGALTSQVHTFPVAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKSNTKV 240
 QY 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTEPYTCVVVDVSHEDP 300
 DB 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTEPYTCVVVDVSHEDP 300
 QY 301 EVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
 DB 301 EVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 13.1295 Seconds
(without alignments)
1704.917 Million cell updates/sec

Title: US-09-758-173-12

Perfect score: 2549

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHNYTKLSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	69.2	330	1 GC1_HUMAN	P01857 homo sapien
2	1600	62.8	326	1 GC2_HUMAN	P01859 homo sapien
3	1586.5	62.2	327	1 GC4_HUMAN	P01861 homo sapien
4	1226.5	48.1	323	1 GC_RABIT	P01870 coryctolagus
5	1212.5	47.6	329	1 GC2_CAVPO	P01862 cavia porce
6	1157	45.4	290	1 GC3_HUMAN	P01860 homo sapien
7	1148	45.0	326	1 GC1_RAT	P20759 rattus norv
8	1142.5	44.8	333	1 GCB_RAT	P20761 rattus norv
9	1138	44.6	324	1 GC1_MOUSE	P01868 mus musculu
10	1137	44.6	329	1 GC3_MOUSE	P22436 mus musculu
11	1133	44.4	393	1 GC1M_MOUSE	P01869 mus musculu
12	1126	44.2	398	1 GC3M_MOUSE	P03987 mus musculu
13	1122	44.0	330	1 GC4A_MOUSE	P01863 mus musculu
14	1119.5	43.9	335	1 GCAB_MOUSE	P01864 mus musculu
15	1117	43.8	329	1 GCAM_MOUSE	P01865 mus musculu
16	1114.5	43.7	399	1 GGC_RAT	P20762 rattus norv
17	1108	43.5	322	1 GCA_RAT	P20760 rattus norv
18	1085	42.6	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.4	405	1 GCBM_MOUSE	P01867 mus musculu
20	489	19.2	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	19.0	429	1 EPC_RAT	P01855 rattus norv
22	465	18.2	421	1 EPC_MOUSE	P06336 mus musculu
23	458	18.0	146	1 HV21_HUMAN	P06331 homo sapien
24	442	17.3	454	1 MUC_HUMAN	P01871 homo sapien
25	437	17.1	458	1 MUC_RABIT	P03988 coryctolagus
26	432.5	17.0	455	1 MUC_MOUSE	P01872 mus musculu
27	427	16.8	479	1 MUCM_RABIT	P04221 coryctolagus
28	425	16.7	457	1 MUC_SUNMU	P20768 suncus muri
29	422.5	16.6	476	1 MUCM_MOUSE	P01873 mus musculu
30	420	16.5	129	1 HV2F_HUMAN	P01824 homo sapien
31	420	16.5	450	1 MUC_CANFA	P01874 canis famil
32	415.5	16.3	454	1 MUC_MESAU	P06337 mesocricetu
33	403	15.8	391	1 MCB_HUMAN	P04220 homo sapien

ALIGNMENTS

RESULT 1

ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human)			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waydal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RN	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RN	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Penstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RL	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RN	chymotryptic peptides of the H-chain, alignment of the tryptic			
RN	peptides and discussion of the complete structure."			
RN	[5]			
RP	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[6]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RP	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P01822 mus musculu
P23085 heterodontu
P23087 heterodontu
P23088 heterodontu
P23084 heterodontu
P01876 homo sapien
P20758 gorilla gor
P01877 homo sapien
P18531 mus musculu
P23086 heterodontu
P01825 homo sapien
P18532 mus musculu

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 [7]
 RN DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 [8]
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RP MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
 CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
 CC MARKER & THE G1M (NON-1) MARKERS.
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 156, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR FIR: A93433; GHU.
 DR PDB: 1FC1; 15-JUL-92.
 DR PDB: 1FC2; 15-JUL-92.
 DR PDB: 1AJ7; 12-NOV-97.
 DR PDB: 1D5B; 09-FEB-00.
 DR PDB: 1D51; 09-FEB-00.
 DR PDB: 1D6V; 04-OCT-00.
 DR PDB: 1DN2; 17-MAY-00.
 DR PDB: 1E4K; 06-JUN-01.
 DR PDB: 1FCC; 20-JUL-95.
 DR PDB: 1H2H; 12-JUN-02.
 DR PDB: 1I72; 08-AUG-01.
 DR PDB: 1IIS; 16-MAY-01.
 DR PDB: 1IIX; 16-MAY-01.
 DR PDB: 1L6X; 10-APR-02.
 DR PDB: 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM: 147100.
 DR GO: GO:0005624; C-membrane fraction; NAS.
 DR GO: GO:0003823; F-antigen binding activity; TAS.
 DR GO: GO:0006955; P-immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS00835; IG-LIKE; 3.
 DR PROSITE: PS00390; IG-MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 FW 3d-structure. 1
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.

FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	
FT	DISULFID	103	103	INTERCHAIN (WITH LIGHT CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	112	112	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	N-LINKED (GLCNAC...).
FT	MOD_RES	330	330	REMOVED POST-TRANSLATIONALLY.
FT	VARIANT	97	97	K -> R (IN GIM(3) MARKER).
FT	VARIANT	239	239	/FTid=VAR_003886.
FT	VARIANT	241	241	D -> E (IN GIM(NON-1) MARKER).
FT	VARIANT	241	241	/FTid=VAR_003887.
FT	VARIANT	241	241	L -> M (IN GIM(NON-1) MARKER).
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	147	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	166	
FT	TURN	168	171	
FT	STRAND	176	179	
FT	TURN	180	181	
FT	STRAND	182	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	260	265	
FT	STRAND	270	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	305	312	
FT	TURN	313	314	
FT	TURN	316	317	
FT	STRAND	320	325	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EEL06C2FA33D CRC64;

Query Match 69.2%; Score 1763; DB 1; Length 330;
 Best Local Similarity 99.7%; Pred. No. 6.5e-114;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	147	ASTKGPSVFFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	206
QY	147	ASTKGPSVFFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	206
Db	1	ASTKGPSVFFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60
QY	207	GLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTKVDKKKSCDKHTCTCPCPAPPELLGG	266
Db	61	GLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTKVDKKKSCDKHTCTCPCPAPPELLGG	120
QY	267	PSVFLFPPKPKDILMISRTPEVTCVVYVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	326
Db	121	PSVFLFPPKPKDILMISRTPEVTCVVYVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	180
QY	327	STYRVSVLTIVLHQDWLNGKEYKCKVKNKALPAPIEKTTISKAGQPRPEQVYTLPSRDE	386
Db	181	STYRVSVLTIVLHQDWLNGKEYKCKVKNKALPAPIEKTTISKAGQPRPEQVYTLPSRDE	240
QY	387	LTRKNOVSLTCLVKGFFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW	446
Db	241	LTRKNOVSLTCLVKGFFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW	300

SUMMARY

```

QY 125 VGMVYNNM-EDVMGPGVLTAVSSASTKGPSVEFLAPSKSTSGTAALGCLVKDYFFPEV 183
Db 119 LQQLISYWFDLWGRGLTAVTSSASTKGPSVEFLAPSKSTSGTAALGCLVKDYFFPEV 178
QY 184 TVSNMGALTSGVHTFPFAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKK 243
Db 179 TVSNMGALTSGVHTFPFAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKK 238
QY 244 AEPKSCDKTHRCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSDEFEV 303
Db 239 VEPKSCDKTHRCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSDEFEV 298
QY 304 FNWYVDGVEVNAKTKPREEQNSTYRYVSVLTVLHODWLNKGYCKVSNKALPAPIEK 363
Db 299 FNWYVDGVEVNAKTKPREEQNSTYRYVSVLTVLHODWLNKGYCKVSNKALPAPIEK 358
QY 364 TISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 423
Db 359 TISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 418
QY 424 PPVLDSGDSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPGK 476
Db 419 PPVLDSGDSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPGK 471

RESULT 2
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueC1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 81.4%; Score 2075; DB 4; Length 473;
Best Local Similarity 83.2%; Pred. No. 1.7e-159;
Matches 397; Conservative 29; Mismatches 39; Indels 12; Gaps 5;

QY 1 MKHLWFFLLVAAPRWLSQVLOESGPGLVKPSSETLSLTCAYSGGSI-SGGYGVGWIRQ 59
Db 8 MKHLWFFLLVAAPRWLSRLOQESGPGLLKPSVTLSTCTVSGDSVASSSYWGVRQ 67
QY 60 PPGKLEWIGFYSSGNGTYNPSLKSQVITSTDTSKNQFSLKNSMTAADTAVYYCVRD 119
Db 68 PPGKLEWIGTI-NFSGNMYSPSLRSRVMTSADMSNSFYKLDSTYAADTAVYYCAAG 126
QY 120 RLFSVGVGVYNNWFDVWGPGVLTAVSSASTKGPSVFLAPSKSTSGTAALGCLVKDYF 179
Db 127 HL--VWGFAGH-----WGQGLVSVSPASTKGPSVFLAPSKSTSESTAAALGCLVKDYF 179
QY 180 PEPVTVSNMGALTSGVHTFPFAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTK 239

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Db 180 PEPVTVSNMGALTSGVHTFPFAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTK 239
QY 240 VDKKAPFKSCDKTHRCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSHED 299
Db 240 VDKRVESK---YGPPCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVDSQED 296
QY 300 PEVKENWYVDGVEVNAKTKPREEQNSTYRYVSVLTVLHODWLNKGYCKVSNKALPA 359
Db 297 PEVQFNWYVDGVEVNAKTKPREEQNSTYRYVSVLTVLHODWLNKGYCKVSNKGLPS 356
QY 360 PIEKTISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENN 419
Db 357 SIEKTISKAGQPREPOVYTLPPSQEEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENN 416
QY 420 YKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPGK 476
Db 417 YKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPGK 473

RESULT 3
Q8N4Y9
ID Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D2E72D6CAA2 CRC64;

Query Match 75.6%; Score 1927.5; DB 4; Length 521;
Best Local Similarity 72.4%; Pred. No. 1.6e-147;
Matches 376; Conservative 32; Mismatches 58; Indels 53; Gaps 5;

QY 7 FILLVAAPRWLSQVLOESGPGLVKPSSETLSLTCAYSGGSI-SGGYGVGWIRQPGKGL 66
Db 7 WLLVYVLOGVQCEQLVDVSGGLVQPGGSLRLSCAASGFIVSDHY-VEMVRQAPGKGP 65
QY 67 WIGSFYSSS--GNTYINPSLKSQVITSTDTSKNQFSLKNSMTAADTAVYYCVRDRLFSV 124
Db 66 WYGCFSKSAHKSTTEVAASVKGRFTILRDDSKNSVHLQMNLSKLTDDTAVYYCVRD--LEG 123
QY 125 VGMVYNNWFDVWGPGVLTAVSSASTKGPSVFLAPSKSTSGTAALGCLVKDYFFPEV 184
Db 124 AGK-YDWYEDINGRGLTVTVSSASTKGPSVFLAPSKSTSGTAALGCLVKDYFFPEV 182
QY 185 VSNMGALTSGVHTFPFAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKA 244
Db 183 VSNMGALTSGVHTFPFAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRV 242
QY 245 -----BPKSCDKTHTCPP 257
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: October 2, 2003, 09:12:09 ; Search time 21.1407 Seconds
(without alignments)
952.662 Million cell updates/sec

Title: US-09-758-173-12

Perfect score: 2549

Sequence:

1 MKHLWFFLLVAAPRWLSQ.....MHEALHNYTKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2549	100.0	476	US-08-487-550-12	Sequence 12, Appl
2	2349	100.0	476	US-09-526-098-12	Sequence 12, Appl
3	2342.5	91.9	473	US-09-049-672A-4	Sequence 4, Appl
4	2309	90.6	476	US-08-487-550-4	Sequence 4, Appl
5	2309	90.6	476	US-09-526-098-4	Sequence 4, Appl
6	2200	86.3	472	US-08-793-450-8	Sequence 8, Appl
7	2153.5	84.5	446	US-08-397-411-7	Sequence 7, Appl
8	2145.5	84.2	467	US-08-523-894-12	Sequence 12, Appl
9	2144.5	84.1	467	US-08-523-894-8	Sequence 8, Appl
10	2137.5	83.9	467	US-08-523-894-10	Sequence 10, Appl
11	2126	83.4	451	US-08-887-352B-18	Sequence 18, Appl
12	2126	83.4	451	US-09-109-207C-18	Sequence 18, Appl
13	2126	83.4	451	US-09-282-505-2	Sequence 2, Appl
14	2126	83.4	451	US-09-054-255-2	Sequence 2, Appl
15	2126	83.4	451	US-09-296-005-18	Sequence 18, Appl
16	2126	83.4	451	US-09-282-846-2	Sequence 2, Appl
17	2126	83.4	451	US-09-680-145-2	Sequence 2, Appl
18	2124	83.3	451	US-08-887-352B-14	Sequence 14, Appl
19	2124	83.3	451	US-08-887-352B-16	Sequence 16, Appl
20	2124	83.3	451	US-08-466-151-65	Sequence 65, Appl
21	2124	83.3	451	US-09-109-207C-14	Sequence 14, Appl
22	2124	83.3	451	US-09-109-207C-16	Sequence 16, Appl
23	2124	83.3	451	US-09-296-005-14	Sequence 14, Appl
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25	2122.5	83.2	475	US-09-740-002-25	Sequence 25, Appl
26	2094.5	82.2	475	US-09-740-002-27	Sequence 27, Appl
27	2093	82.1	453	US-08-466-151-8	Sequence 8, Appl

28 2093 82.1 453 4 US-08-466-163B-8 Sequence 8, Appl
29 2072.5 81.3 462 4 US-09-289-942A-7 Sequence 7, Appl
30 2071.5 81.3 452 3 US-09-027-449-71 Sequence 71, Appl
31 2071.5 81.3 452 3 US-09-026-985-71 Sequence 71, Appl
32 2071.5 81.3 452 4 US-09-121-952A-71 Sequence 71, Appl
33 2071.5 81.3 452 4 US-09-234-340A-71 Sequence 71, Appl
34 2063 80.9 476 2 US-08-378-939-10 Sequence 10, Appl
35 2053.5 80.6 449 4 US-09-679-397-2 Sequence 2, Appl
36 2053.5 80.6 449 4 US-09-680-148-2 Sequence 2, Appl
37 2053.5 80.6 449 4 US-09-304-465A-2 Sequence 2, Appl
38 2053.5 80.6 459 1 US-08-157-101A-7 Sequence 7, Appl
39 2053 80.5 478 3 US-08-487-550-8 Sequence 8, Appl
40 2053 80.5 478 4 US-09-526-098-8 Sequence 8, Appl
41 2033 79.8 449 1 US-08-458-516-13 Sequence 13, Appl
42 2024.5 79.4 467 3 US-09-049-672A-8 Sequence 8, Appl
43 2016.5 79.1 454 2 US-07-934-373C-22 Sequence 22, Appl
44 2016.5 79.1 454 3 US-08-437-642B-22 Sequence 22, Appl
45 2016.5 79.1 454 4 US-08-146-206C-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: 'MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS'

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,550

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 476 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-487-550-12

Query Match

Best Local Similarity 100.0%; Score 2549; DB 3; Length 476;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKHLWFFLLVAAPRWLSQVQLQESGPGLVKVPSEFSLTCAVSGSISGGYGGWIRQP 60
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DB 121 LFSVVGMYNNWFDVWPGVLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
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DB 241 DKAEKPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
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DB 301 EVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAP 360
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DB 361 IEKTTISKAGQPREPQVYITLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNY 420
QY 421 KTTTPVLDSDGSEFFLYSKLTVDKSRWQGNFVSCVMHEALHNHYTQKSLSLSPGK 476
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RESULT 2
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; Sequence 12, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMARIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELEPHONE: 703-835-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-09-526-098-12
Query Match 100.0%; Score 2549; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.5e-198;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MKHLWPELLVAAPRWVLSQVQLQESGPGLVKPSSETLSLTCAVSGGSGISGGYGVGWIRQP 60
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DB 61 PKGLEWIGSFYSSSGNTYYNPSLKSQVITSTDTSKNQFSLKLNMTAADTAVYCYVDR 120
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QY 421 KTTTPVLDSDGSEFFLYSKLTVDKSRWQGNFVSCVMHEALHNHYTQKSLSLSPGK 476
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RESULT 3
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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(without alignments)
421.442 Million cell updates/sec

Title: US-09-758-173-12

Perfect score: 2549

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Scoring table: BLOSUM62

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2309	90.6	476	10	US-09-948-429B-4
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7	2309	90.6	476	12	US-10-291-532-4
8	2309	90.6	476	14	US-10-124-905-4
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10	2144.5	84.1	467	15	US-10-211-357-8
11	2138	83.9	580	12	US-10-310-719-37
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13	2127	83.4	451	11	US-09-925-179-66
14	2126	83.4	451	9	US-09-920-171-18
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42	2117.5	83.1	450	9	US-09-796-848A-45
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44	2117.5	83.1	450	10	US-09-996-288-252
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ALIGNMENTS

RESULT 1

US-09-948-429B-12
; Sequence 12, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:

APPLICANT: Anderson, Dorell R.

TITLE OF INVENTION: 'MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/948,429B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-429B-12

Query Match 100.0%; Score 2549; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-172;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKHLWFFLLVAAPRWVLSQVQLQESGPGILVQPKSETLSLTCAVSGGSISSGGYGGWIRQP 60
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DB 61 PKGLEWIGSFYSSSGNTYINPFLSKQVITSTDTSKNQFSLKLNMTAADTAVYICVDR 120
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DB 181 EPTVSNWNSGALTSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240
QY 241 DKAEPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 361 IEKTIKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSGPK 476
DB 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSGPK 476

RESULT 2
US-10-124-807-12
Sequence 12, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dartell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124.807
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE: 09/08/97
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-124-807-12

Query Match 100.0%; Score 2549; DB 12; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-172;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWVLSQVQLQESGPGILVQPKSETLSLTCAVSGGSISSGGYGGWIRQP 60
DB 1 MKHLWFFLLVAAPRWVLSQVQLQESGPGILVQPKSETLSLTCAVSGGSISSGGYGGWIRQP 60
QY 61 PKGLEWIGSFYSSSGNTYINPFLSKQVITSTDTSKNQFSLKLNMTAADTAVYICVDR 120
DB 61 PKGLEWIGSFYSSSGNTYINPFLSKQVITSTDTSKNQFSLKLNMTAADTAVYICVDR 120
QY 121 LFSVVGMYNNWEDVWGPGVLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 LFSVVGMYNNWEDVWGPGVLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 181 EPTVSNWNSGALTSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240
DB 181 EPTVSNWNSGALTSGVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240
QY 241 DKAEPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 361 IEKTIKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSGPK 476
DB 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSGPK 476

RESULT 3
US-10-291-532-12
Sequence 12, Application US/10291532
Publication No. US20030180290A1
GENERAL INFORMATION:
APPLICANT: HARIHARAN, KANDASAMY
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REFERENCE: 037003/291872
CURRENT APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/331,187
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 09/758,173

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:10:05 ; Search time 37.4695 Seconds
(without alignments)
8304.972 Million cell updates/sec

Title: US-09-758-173-1

Perfect score: 705

Sequence: 1 ATGAGGGTCCCGCTCAGCT.....CCCTACAGATTGTCATGA 705

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2.6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2.6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2.6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2.6/ptodata/2/ina/PTCUS_COMB.seq.*
- 6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	705	100.0	705	3	US-08-487-550-1
2	705	100.0	705	4	US-09-526-098-1
3	585.2	83.0	702	3	US-08-523-894-5
4	540.2	76.6	711	3	US-08-487-550-9
5	540.2	76.6	711	4	US-09-526-098-9
6	473	67.1	935	3	US-09-043-672A-20
7	457	64.8	902	2	US-08-378-939-11
8	456	64.7	895	3	US-09-049-672A-25
9	455.4	64.6	891	3	US-09-049-672A-23
10	440	62.4	705	4	US-09-372-425A-3
11	435.6	61.8	885	4	US-09-152-060-47
12	434	61.6	879	4	US-09-152-060-29
13	432.2	61.3	928	4	US-09-152-060-46
14	425.4	60.3	919	3	US-09-049-672A-24
15	407.4	57.8	716	4	US-08-793-450-5
16	392.4	55.7	491	4	US-09-702-705-833
17	392.4	55.7	491	4	US-09-736-457-833
18	388.2	55.1	805	4	US-09-620-312D-62
19	387.4	55.0	608	4	US-09-702-705-908
20	387.4	55.0	608	4	US-09-736-457-908
21	375	53.2	543	4	US-09-702-705-970
22	375	53.2	543	4	US-09-736-457-970
23	340.2	48.3	420	4	US-09-702-705-433
24	340.2	48.3	420	4	US-09-736-457-433
25	317	45.0	373	4	US-09-702-705-1625
26	317	45.0	373	4	US-09-736-457-1625
27	311.4	44.2	705	4	US-09-592-998C-7

C 28	306.6	43.5	584	4	US-09-404-879A-268	Sequence 268, App
C 29	306.6	43.5	584	4	US-09-338-933-268	Sequence 268, App
C 30	306.6	43.5	584	4	US-09-215-681-268	Sequence 268, App
C 31	291.8	41.4	361	4	US-09-702-705-1589	Sequence 1589, App
C 32	291.8	41.4	361	4	US-09-736-457-1589	Sequence 1589, App
C 33	282.8	40.1	329	4	US-09-702-705-409	Sequence 409, App
C 34	282.8	40.1	329	4	US-09-736-457-409	Sequence 409, App
C 35	273.2	38.8	771	3	US-08-991-789A-241	Sequence 241, App
C 36	273.2	38.8	771	4	US-09-062-451-241	Sequence 241, App
C 37	273.2	38.8	771	4	US-09-598-326-241	Sequence 241, App
C 38	273.2	38.8	771	4	US-09-283-198-241	Sequence 241, App
C 39	267.2	37.9	387	1	US-08-379-072A-20	Sequence 20, Appl
C 40	267.2	37.9	387	1	US-08-478-039-109	Sequence 109, Appl
C 41	267.2	37.9	387	1	US-08-481-869-20	Sequence 20, Appl
C 42	267.2	37.9	387	1	US-08-476-349A-109	Sequence 109, Appl
C 43	267.2	37.9	387	1	US-08-476-237-16	Sequence 16, Appl
C 44	267.2	37.9	387	3	US-08-523-894-3	Sequence 3, Appl
C 45	263	37.3	585	4	US-09-620-312D-551	Sequence 551, App

ALIGNMENTS

RESULT 1
US-08-487-550-1
; Sequence 1, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..705
; US-08-487-550-1

Query Match 100.0%; Score 705; DB 3; Length 705;

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run On: October 2, 2003, 13:05:20 ; Search time 1165.91 Seconds
(without alignments)
14695.420 Million cell updates/sec

Title: US-09-758-173-1
Perfect score: 705
Sequence: 1 ATGAGGTCCTCCCTCAGCT.....CCCTACAGATGTTCAIGA 705

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
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 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_esti:*
 - 10: gb_est2:*
 - 11: gb_est3:*
 - 12: gb_est4:*
 - 13: gb_est5:*
 - 14: gb_est6:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pin:*
 - 20: em_gss_vit:*
 - 21: em_gss_fun:*
 - 22: em_gss_mam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558.8	79.3	952	13	BQ711447
2	555.6	78.8	931	13	BQ709526
3	555.2	78.8	931	13	BQ711683
4	552	78.3	796	10	BQ757730

5	552	78.3	969	13	BQ707953	BQ707953
6	551.2	78.2	921	13	BQ708246	BQ708246
7	548.8	77.8	920	13	BQ712280	BQ712280
8	547.2	77.6	925	13	BQ710672	BQ710672
9	546	77.4	832	10	BQ746204	BQ746204
10	545.8	77.4	908	13	BQ884067	BQ884067
11	545.6	77.4	754	12	B1907909	B1907909
12	545.2	77.3	924	10	BQ756256	BQ756256
13	545	77.3	1086	12	BM924274	BM924274
14	544.4	77.2	917	13	BQ711587	BQ711587
15	542.4	76.9	949	13	BQ709509	BQ709509
16	541.6	76.8	1018	12	BM914338	BM914338
17	540.8	76.7	947	13	BQ709579	BQ709579
18	540.4	76.7	789	12	B1765865	B1765865
19	538	76.3	645	14	CB553601	CB553601
20	537	76.2	742	12	B1906298	B1906298
21	533.6	75.7	874	10	BQ753301	BQ753301
22	531	75.3	837	10	BQ754193	BQ754193
23	530.2	75.2	731	9	AV649126	AV649126
24	529.4	75.1	670	14	CB554958	CB554958
25	529	75.0	803	10	BQ758687	BQ758687
26	528	74.9	862	10	BF338816	BF338816
27	527.4	74.8	842	10	BQ686249	BQ686249
28	526	74.6	1201	13	BX377262	BX377262
29	525.6	74.5	788	12	BM007725	BM007725
30	525	74.5	1010	12	BM914307	BM914307
31	520.8	73.9	913	10	BQ745387	BQ745387
32	520.2	73.8	871	10	BQ398521	BQ398521
33	517.2	73.4	1005	10	BF974359	BF974359
34	516.6	73.3	883	12	B1760703	B1760703
35	515.2	73.1	926	12	B1911261	B1911261
36	513.8	72.9	868	10	BQ745881	BQ745881
37	512.8	72.7	923	13	BQ708365	BQ708365
38	512.6	72.7	864	10	BQ756128	BQ756128
39	510	72.3	958	13	B146944	B146944
40	508.4	72.1	782	12	BM007795	BM007795
41	508.2	72.1	801	12	BM007626	BM007626
42	508	72.1	829	10	BQ754011	BQ754011
43	507.8	72.0	973	13	BX370978	BX370978
44	501.8	71.2	688	10	BQ745481	BQ745481
45	499.8	70.9	722	13	BQ576097	BQ576097

ALIGNMENTS

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LOCUS BQ711447
DEFINITION AGENCOURT_8353624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279618
5', mRNA sequence.
ACCESSION BQ711447
VERSION BQ711447.1 GI:21850346
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 952)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM2469 row: h column: 19
High quality sequence stop: 584.

952 bp mRNA linear EST 16-JUL-2002
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BQ712280 AGENCOURT
BQ710672 AGENCOURT
BQ746204 602723726
BQ884067 AGENCOURT
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BQ686249 602638157
BX377262 BX377262
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BQ576097 UI-H-521-

XX	WPI; 1997-108638/10.
DR	P-PSDB; AAQ01817.
XX	
PT	Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
XX	useful for treating autoimmune disease or graft-versus-host disease
PS	Claim 7; Fig 8A; 8lpp; English.
XX	
CC	2 DNA sequences (AAAT62509 and AAT62510) respectively code for
CC	primatised forms (AAW01817 and AAQ01818) of the light and heavy chains
CC	of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC	7C10. Cloned 7C10 light and heavy variable genes are inserted into
CC	an expression vector (pref. NEOSPLA) which contains human light and
CC	heavy chain constant region genes to allow prodn. of primatised
CC	antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC	antibodies have also been produced (see also AAQ01819-22). The
CC	primatised antibodies inhibit the B7:CD28 pathway, making them
CC	useful immunosuppressants for the treatment of autoimmune disorders
CC	and graft-versus-host disease.
XX	
SQ	Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;
	Query Match 100.0%; Score 705; DB 18; Length 705;
	Best Local Similarity 100.0%; Pred. No. 4.3e-167;
	Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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QY	421 CGGCCCCCTCTGAGGAGCTTCAAGCCACAAGGCCACACTGGTGTCTATAAGTGAC 480
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QY	481 TTCTACCCGGAGCCGTGACAGTGGCTTGAAGGCAGATAGCAGCCCTCAAGCGCGGA 540
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QY	541 GTGGAGACCCACACACCTCCAAACAAGCAACAAGTACGCGGCCAGCAGCTACCTG 600
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QY	601 AGCCTGAGCCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTCACGCATGAA 660
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Db	
QY	661 GGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAAATGTTATGA 705
Db	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 2, 2003, 12:12:30 ; Search time 144.396 Seconds
(without alignments)
13179.730 Million cell updates/sec

Title: US-09-758-173-1

Perfect score: 705

Sequence: 1 ATGAGGTCGCCGCTCAGCT.....CCCTACAGATGTTTCATGA 705

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	18	Primates anti-hu
2	705	100.0	705	19	Macaque primates
3	705	100.0	705	24	DNA sequence of a
4	585.2	83.0	702	18	Ant-CD4 monkey-hu
5	582.6	82.6	926	20	Human bladder tumo
6	558.6	79.2	699	25	DNA encoding monoc
7	555.6	78.8	836	23	DNA encoding novel
8	540.2	76.6	711	19	Macaque primates

9	540.2	76.6	711	24	AAS17246	DNA sequence of a
10	538.6	76.4	711	18	AA62512	Primates anti-hu
11	527.6	74.8	1027	24	ABO54438	Human ovarian anti
12	524	74.3	841	23	AA583486	DNA encoding novel
13	520.8	73.9	904	24	ABK28671	Human cDNA encodin
14	520.4	73.8	869	22	AAS22717	Human cDNA encodin
15	518	73.5	702	24	ABK67760	DNA encoding antib
16	516.4	73.2	830	25	ABT31878	DNA encoding human
17	516.4	73.2	830	25	ABT31878	Anti-CD40 monoclon
18	516	73.2	791	23	AAS87271	DNA encoding novel
19	515	73.0	1825	22	AAS22777	Human cDNA encodin
20	514.4	73.0	859	22	AAS22481	Human cDNA encodin
21	512.8	72.7	960	21	AACT8188	Human cancer assoc
22	512	72.6	872	9	AA81655	VDJC regions of hu
23	511	72.5	654	22	AAS13364	Human cDNA encodin
24	509.2	72.2	930	22	AAS22541	Human cDNA encodin
25	506	71.8	793	23	AAS83481	DNA encoding novel
26	504	71.5	807	23	AA83484	DNA encoding novel
27	495.2	70.2	863	24	ABK28650	Human cDNA encodin
28	490	69.5	886	24	ABQ93531	Human cDNA SEQ ID
29	480	68.1	849	22	AAH98186	Human EST-derived
30	475.8	67.5	870	24	AAH50812	Human cancer statu
31	474.2	67.3	884	11	AAQ03609	Sequence encoding
32	473.6	67.2	810	23	AAS87270	Human immune syste
33	473	67.1	935	22	AA65525	DNA encoding novel
34	472	67.0	768	20	AA65525	Monoclonal antibod
35	472	67.0	768	20	AA65525	Monoclonal antibod
36	465.6	66.0	826	22	AAH58109	Human polynucleoti
37	462.8	65.6	915	24	ABN97248	Gene #3746 used to
38	462.8	65.6	915	24	ABK64815	Lung cancer relate
39	462.8	65.6	915	24	ABL65478	Human cDNA SEQ ID
40	462.8	65.6	964	24	ABQ93374	Anti-HIV-1 recombi
41	462.2	65.6	654	14	AAQ9835	Plasmid Glambda-1B
42	462	65.5	762	22	AAQ84209	Plasmid Glambda-1A
43	462	65.5	5679	22	AA67073	DNA encoding novel
44	461.8	65.5	889	23	AAS77073	Antibody D lambda
45	457	64.8	902	14	AAQ35100	

ALIGNMENTS

RESULT 1
AA62509
ID AA62509 standard; DNA; 705 BP.

XX AA62509;

AC AA62509;

DT 25-MAY-1997 (first entry)

XX 25-MAY-1997 (first entry)

XX Primates anti-human B7.1 antigen antibody 7c10 light chain DNA.

XX Monoclonal antibody; cynomolgus monkey; macaque; 7C10;

XX Primates anti-human B7.1 antigen; CD28; immunosuppressive;

XX autoimmune disease; idiopathic thrombocytopenia purpura;

XX systemic lupus erythematosus; rheumatoid arthritis; psoriasis;

XX type 1 diabetes mellitus; graft versus host disease;

XX hetero-hybridoma; transfection; ss.

XX Chimeric Macaca cynomolgus;

XX Chimeric Homo sapiens.

XX WO9640878-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US10053.

XX 07-JUN-1995; 95US-0487550.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brans P, Hanna N, Shetowsky WS;

FEATURES
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BASE COUNT 162 a 214 c 207 g 122 t
ORIGIN

Query Match 100.0%; Score 705; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ACCTGTGGGGAGACACAGTAGAATATGTCTCCACTGGTACCAGAGAGCCAGCG 180
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QY 181 CGGGCCCCCTATCTGCTCATCTATGATGATAGTACCGGCCCTCAGGATCCCTGAGCGA 240
DB 181 CGGGCCCCCTATCTGCTCATCTATGATGATAGTACCGGCCCTCAGGATCCCTGAGCGA 240

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QY 301 GATGAGGCTGACTATTACTGTGCTGAGTGTGGGACAGGCTAGTATCATCCGGTCTTCGGA 360
DB 301 GATGAGGCTGACTATTACTGTGCTGAGTGTGGGACAGGCTAGTATCATCCGGTCTTCGGA 360

QY 361 GGAGGACCCGGGTGACCGTCTAGTGTGACCCAAAGCTGCGCCCTCGGTCACTCTGTTTC 420
DB 361 GGAGGACCCGGGTGACCGTCTAGTGTGACCCAAAGCTGCGCCCTCGGTCACTCTGTTTC 420

QY 421 CCGCCCTCTCTGAGGAGCTTCAAGCCAAAGCCACATGAGTGTCTCTATAAGTGAC 480
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QY 541 GTGAGACCCACACCCCTCCAAACAAAGCAACAAAGTACCGGGCCAGCTACCTG 600
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QY 661 GGGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCATGA 705
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RESULT 2
LOCUS AR265196 705 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6492134.
ACCESSION AR265196
VERSION AR265196.1 GI:29693617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 705)
AUTHORS Aquin,S. and Vezina,Louis..P.
TITLE Method for producing polyhydroxyalkanoates in recombinant organisms
JOURNAL Patent: US 6492134-A 1 10-DEC-2002;

FEATURES
source
BASE COUNT 162 a 214 c 207 g 122 t
ORIGIN

Query Match 100.0%; Score 705; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCTCTGGGGCTCTCTGGTCTCTGGTCCGAGGTGCAGATGT 60
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QY 61 GCCTATGAAGTACTCAGCCACCCTCGGTGTCTGGTCTCTGGTCCGAGGTGCAGATGT 120
DB 61 GCCTATGAAGTACTCAGCCACCCTCGGTGTCTGGTCTCTGGTCCGAGGTGCAGATGT 120

QY 121 ACCTGTGGGGAGACACAGTAGAATATGTCTCCACTGGTACCAGAGAGCCAGCG 180
DB 121 ACCTGTGGGGAGACACAGTAGAATATGTCTCCACTGGTACCAGAGAGCCAGCG 180

QY 181 CGGGCCCCCTATCTGCTCATCTATGATGATAGTACCGGCCCTCAGGATCCCTGAGCGA 240
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QY 301 GATGAGGCTGACTATTACTGTGCTGAGTGTGGGACAGGCTAGTATCATCCGGTCTTCGGA 360
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QY 361 GGAGGACCCGGGTGACCGTCTAGTGTGACCCAAAGCTGCGCCCTCGGTCACTCTGTTTC 420
DB 361 GGAGGACCCGGGTGACCGTCTAGTGTGACCCAAAGCTGCGCCCTCGGTCACTCTGTTTC 420

QY 421 CCGCCCTCTCTGAGGAGCTTCAAGCCAAAGCCACATGAGTGTCTCTATAAGTGAC 480
DB 421 CCGCCCTCTCTGAGGAGCTTCAAGCCAAAGCCACATGAGTGTCTCTATAAGTGAC 480

QY 481 TTCTACCCGGAGCGGTGACAGTGGCTGGAAGCCAGATAGCAGCCCGCTCAAGGGGGA 540
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QY 661 GGGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCATGA 705
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RESULT 3
LOCUS BD063034 705 bp DNA linear PAT 27-AUG-2002
DEFINITION Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
ACCESSION BD063034
VERSION BD063034.1 GI:22608637
KEYWORDS JP 2001504693-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 705)
AUTHORS Anderson,D.R., Hanna,N., Brama,P. and Hard,C.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 ; Search time 1851.84 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-1
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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16	529.6	75.1	824	9	AB064176	AB064176 Homo sapi
17	526.4	74.7	813	9	AB064167	AB064167 Homo sapi
18	525.2	74.5	895	9	BC022823	BC022823 Homo sapi
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28	512	72.6	798	9	AB064184	AB064184 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS ARI08862
DEFINITION Sequence 1 from patent US 6113898.
ACCESSION ARI08862
VERSION ARI08862.1 GI:12825138
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 705)
AUTHORS Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
JOURNAL Patent: US 6113898-A 1 05-SEP-2000;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: October 2, 2003, 19:53:01 ; Search time 139.466 Seconds
(without alignments)
12894.584 Million cell updates/sec

Title: US-09-758-173-1
Perfect score: 705
Sequence: 1 ATGAGGGTCCCGCTCAGT.....CCCTACAGATGTCATGA 705

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues
Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications,NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Length	ID	Description
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3	705	100.0	705	12	Sequence 1, Appl
4	705	100.0	705	13	Sequence 1, Appl
5	705	100.0	705	13	Sequence 1, Appl
6	585.2	83.0	702	14	Sequence 5, Appl
7	588.6	79.2	699	12	Sequence 11, Appl
8	555	78.7	1402	14	Sequence 12610, A
9	552.6	78.4	642	11	Sequence 95, Appl
10	540.2	76.6	711	12	Sequence 9, Appl
11	540.2	76.6	711	12	Sequence 9, Appl
12	540.2	76.6	711	13	Sequence 9, Appl
13	540.2	76.6	711	13	Sequence 9, Appl
14	539.6	76.5	1590	14	Sequence 5, Appl
15	539.6	76.5	1590	14	Sequence 5, Appl
16	530	75.2	868	9	Sequence 157, App

SUMMARIES

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c 18	516	73.2	859	14	US-10-198-846-13995	Sequence 13995, A
c 19	512.8	72.7	960	9	US-09-925-301-582	Sequence 582, App
20	511	72.5	654	11	US-09-791-153A-50	Sequence 50, Appl
21	510.6	72.4	2667	14	US-10-158-646-76	Sequence 76, Appl
c 22	505.6	71.7	895	14	US-10-198-846-12838	Sequence 12838, A
c 23	501.6	71.1	830	10	US-09-981-353-42	Sequence 42, Appl
c 24	494	70.1	849	14	US-10-198-846-12585	Sequence 12585, A
25	492.6	69.9	636	11	US-09-972-656-97	Sequence 97, Appl
26	488.6	69.3	846	10	US-09-981-353-55	Sequence 55, Appl
27	487	69.1	1480	10	US-09-981-353-1146	Sequence 146, App
28	473.8	67.2	857	9	US-09-822-849A-158	Sequence 158, App
29	472	67.0	768	10	US-09-747-669-4	Sequence 4, Appl
c 30	472	67.0	768	10	US-09-747-669-5	Sequence 5, Appl
31	472	67.0	768	14	US-10-290-703-4	Sequence 4, Appl
32	472	67.0	768	14	US-10-290-703-5	Sequence 5, Appl
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34	469.4	66.6	1640	14	US-10-198-846-13206	Sequence 13206, A
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c 36	465	66.0	1640	14	US-10-198-846-13206	Sequence 13206, A
37	463.2	65.7	848	14	US-10-158-646-70	Sequence 70, Appl
38	463	65.7	888	14	US-10-158-646-71	Sequence 71, Appl
39	462.8	65.6	915	10	US-09-954-456-788	Sequence 788, App
40	462.8	65.6	915	10	US-09-880-107-3743	Sequence 3743, App
41	462.8	65.6	915	12	US-09-873-319-710	Sequence 710, App
42	462.8	65.6	915	12	US-09-960-706-1069	Sequence 1069, App
43	461.8	65.5	883	14	US-10-158-646-73	Sequence 73, Appl
44	457.2	64.9	870	11	US-09-968-433-40	Sequence 40, Appl
45	456	64.7	2635	14	US-10-198-846-13529	Sequence 13529, A

ALIGNMENTS

RESULT 1

US-09-948-429B-1

; Sequence 1, Application US/09948429B

; Patent No. US20020177689A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/948,429B

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 : Search time 27.4586 seconds
(without alignments)
1352.654 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPAQLGLLLWLPQARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1243	100.0	234	AAW01817	Primatized anti-hu
2	1243	100.0	234	AAW63760	Macaque primatized
3	1243	100.0	234	AAU11538	Protein sequence o
4	1015.5	81.7	233	AAW14924	Ant-CD4 monkey-hu
5	1001	80.5	232	ABU08020	Monoclonal rabies
6	931.5	79.8	247	ABG19295	Novel human diagno
7	979	78.8	238	ABG19299	Novel human diagno
8	976.5	78.6	232	AAU14412	Human novel protei
9	973	78.3	236	AAW63764	Macaque primatized

10	973	78.3	236	AAU11645	Protein sequence o
11	973	78.3	269	ABF41361	Human ovarian anti
12	970	78.0	236	AAW01821	Primatized anti-hu
13	967.5	77.8	212	ABR01497	Human anti-TIMP-1
14	966	77.7	213	ABR01474	Human anti-TIMP-1
15	960.5	77.3	212	ABR01489	Human anti-TIMP-1
16	959	77.2	231	AAU14176	Human novel protei
17	959	77.2	234	ABG23084	Novel human diagno
18	958.5	77.1	232	AAU14236	Human novel protei
19	958	77.1	211	ABR01495	Human anti-TIMP-1
20	956.5	77.0	212	ABR01486	Human anti-TIMP-1
21	955	76.8	235	ABP63052	Human polypeptide
22	953	76.7	211	ABR01472	Human anti-TIMP-1
23	951	76.5	211	ABR01471	Human anti-TIMP-1
24	946	76.1	231	ABJ36936	Anti-CD40 monoclon
25	944	75.9	218	AAU08381	Anti-OFGBP antibod
26	944	75.9	233	AAU82012	Human secreted pro
27	939.5	75.6	236	AAU14472	Human novel protei
28	936.5	75.3	244	AAU43979	Human cancer assoc
29	936	75.3	226	ABG19294	Novel human diagno
30	934	75.1	233	ABG91843	Human antibody fra
31	934	75.1	233	ABG78152	Human Fv molecule
32	925	74.4	233	AAU81260	VDJC regions of hu
33	915	73.6	233	ABG92022	Antibody protein #
34	912	73.4	231	AAU81991	Human secreted pro
35	906.5	72.9	232	AAU23527	Human EST encoded
36	905	72.8	238	ABG19297	Novel human diagno
37	898.5	72.3	246	ABJ12413	Human bone marrow
38	890.5	71.6	216	ABR01473	Human anti-TIMP-1
39	890	71.6	242	ABU08021	Monoclonal rabies
40	886	71.3	234	ABG73422	Human IgG anti-rhe
41	885.5	71.2	216	ABR01482	Human anti-TIMP-1
42	885	71.2	215	ABR01493	Human anti-TIMP-1
43	885	71.2	215	ABR01496	Human anti-TIMP-1
44	884.5	71.2	217	AAU42163	Anti-HIV-1 recombi
45	881	70.9	236	ABG23083	Novel human diagno

ALIGNMENTS

RESULT 1
AAW01817
ID AAW01817 standard; Protein; 234 AA.
XX AAW01817;
AC AC
XX 25-MAY-1997 (first entry)
DT DT
XX Primatized anti-human B7.1 antigen antibody 7C10 light chain.
DE DE
XX Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW Primatized antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX XX
PN W09640878-A1.
XX 19-DEC-1996.
XX XX
PF 06-JUN-1996; 96WO-US10053.
XX XX
PR 07-JUN-1995; 95US-0487550.
XX XX
PA (IDEC-) IDEC PHARM CORP.
XX XX
PI Anderson DR, Brans P, Hanna N, Shestowsky WS;
XX XX

DR WPI; 1997-108638/10.
 DR N-PSDB; AAT62509.
 XX
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen
 PT useful for treating autoimmune disease or graft-versus-host disease
 XX
 PS Claim 6; Fig 8A; 81pp; English.
 XX
 CC 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
 CC variable genes (see also AAT62509 and AAT62510) are inserted into
 CC an expression vector (pref. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
 CC antibodies have also been produced (see also AAW01819-22). The
 CC primatised antibodies inhibit the B7:CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.
 XX
 SQ Sequence 234 AA;
 Query Match 100.0%; Score 1243; DB 18; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1e-70;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRVPAQLLGLLLLPAGARCAVELTPPSVSPGQTARITCGDNRNRYVHWYQKPA 60
 DB 1 MRVPAQLLGLLLLPAGARCAVELTPPSVSPGQTARITCGDNRNRYVHWYQKPA 60
 QY 61 RAPILVIYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYICQVWDRASDPVFG 120
 DB 61 RAPILVIYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYICQVWDRASDPVFG 120
 QY 121 GGTRTVTLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVANKADSPVKAG 180
 DB 121 GGTRTVTLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVANKADSPVKAG 180
 QY 181 VETTPSKQSNKYYAASSYLSLTPEQWKSQRSYSCQVTHEGSTVEKTVAPTECS 234
 DB 181 VETTPSKQSNKYYAASSYLSLTPEQWKSQRSYSCQVTHEGSTVEKTVAPTECS 234
 RESULT 2
 AAW63760
 ID AAW63760 standard; Protein; 234 AA.
 AC AAW63760;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primatised 7C10 light chain protein.
 XX
 KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation.
 XX
 OS Macaca fascicularis.
 XX
 PN W09819706-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 29-OCT-1997; 97WO-US19906.
 XX
 PR 08-NOV-1996; 96US-0746361.
 XX
 FA (IDEC-) IDEC PHARM CORP.
 XX
 FI Anderson DR, Brams P, Hanna N;
 XX

DR WPI; 1998-286601/25.
 DR N-PSDB; AAV35484.
 XX
 PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 PS Example 7; Fig 3a; 87pp; English.
 XX
 CC This sequence represents a primatised form of the antibody 7C10 light
 CC chain from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 234 AA;
 Query Match 100.0%; Score 1243; DB 19; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1e-70;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRVPAQLLGLLLLPAGARCAVELTPPSVSPGQTARITCGDNRNRYVHWYQKPA 60
 DB 1 MRVPAQLLGLLLLPAGARCAVELTPPSVSPGQTARITCGDNRNRYVHWYQKPA 60
 QY 61 RAPILVIYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYICQVWDRASDPVFG 120
 DB 61 RAPILVIYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYICQVWDRASDPVFG 120
 QY 121 GGTRTVTLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVANKADSPVKAG 180
 DB 121 GGTRTVTLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVANKADSPVKAG 180
 QY 181 VETTPSKQSNKYYAASSYLSLTPEQWKSQRSYSCQVTHEGSTVEKTVAPTECS 234
 DB 181 VETTPSKQSNKYYAASSYLSLTPEQWKSQRSYSCQVTHEGSTVEKTVAPTECS 234
 RESULT 3
 AAU11538
 ID AAU11538 standard; Protein; 234 AA.
 XX
 AC AAU11538;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Protein sequence of primatised form of the light chain of 7C10 antibody.
 XX
 KW Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.

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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:07:34 ; Search time 10.2833 seconds
(without alignments)
2188.349 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
Sequence: 1 MRVPAQLGLLLWLPQARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.76:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1016	81.7	232	2 S25756	Ig lambda chain -
2	1012.5	81.5	233	2 S25747	Ig lambda chain -
3	979	78.8	231	2 S25738	Ig lambda chain -
4	959	77.2	231	2 S25751	Ig lambda chain -
5	939	77.2	231	2 S25753	Ig lambda chain -
6	936	75.3	226	2 S25745	Ig lambda chain -
7	923	74.3	213	2 JE0247	Ig lambda chain NI
8	920	74.0	233	2 S25748	Ig lambda chain
9	920	74.0	235	2 S05270	Ig lambda chain pr
10	910	73.2	232	2 S25742	Ig lambda chain -
11	905	72.8	233	2 S25741	Ig lambda chain -
12	883	71.0	233	2 S25752	Ig lambda chain -
13	881	70.9	235	2 S25750	Ig lambda chain -
14	873	70.2	234	2 S25757	Ig lambda chain -
15	871.5	70.1	213	2 S21066	Ig lambda chain -
16	871.5	70.1	236	2 S25746	Ig lambda chain V
17	870	70.0	233	2 S25744	Ig lambda chain -
18	870	70.0	235	2 S14675	Ig lambda chain -
19	867.5	69.8	235	2 S25759	Ig lambda chain -
20	867	69.8	235	2 S25759	Ig lambda chain -
21	862.5	69.4	217	2 A42193	Ig lambda chain (B
22	859	69.1	216	2 JE0246	Ig lambda chain NI
23	850.5	68.4	235	2 S29258	Ig lambda chain V
24	846	68.1	216	2 S25754	Ig lambda chain (K
25	840.5	67.6	235	2 S03401	Ig lambda chain -
26	835	67.2	190	2 S25758	Ig lambda chain -
27	833.5	67.1	212	2 S25740	Ig lambda chain -
28	822	66.1	216	2 S70431	Ig lambda chain -
29	820.5	66.0	235	2 JE0245	Ig lambda chain NI
				2 S25749	Ig lambda chain -

ALIGNMENTS

RESULT 1

S25756
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25756
R:Combratio, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25756
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-232 <COM>
A:Cross-references: EMBL:X57821; NID:g33741; PID:CAA40958.1; PID:g33742
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:147-215/Domain: immunoglobulin homology <IMM>

Query Match	81.7%	Score	1016	DB	2	Length	232
Best Local Similarity	86.0%	Pred. No.	8.7e-61				
Matches	196	Conservative	14	Mismatches	16	Indels	2
Gaps	2						
QY	7	LLGLLLLP	PGARCA	YELTQ	PPSVS	PGQTAR	ITCGD
Db	7	LLG-LLSH	CGTSVT	SYVLT	QPPSV	SVAPG	KTASIT
QY	67	IYDDSD	RPSGIP	PERFSG	SGKSGN	TATLT	INGVE
Db	66	IYDDSD	RPSGIP	PERFSG	SGKSGN	TATLT	INGVE
QY	127	VLGQPKA	APSVT	LFPPS	SEELQ	ANKAT	LVCLIS
Db	125	VLGQPKA	APSVT	LFPPS	SEELQ	ANKAT	LVCLIS
QY	187	SKQSNKY	AAASSY	LSLTPE	QWKS	HRSYSC	QVTH
Db	185	SKQSNKY	AAASSY	LSLTPE	QWKS	HRSYSC	QVTH

RESULT 2

S25747
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25747
R:Combratio, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25747
A:Status: preliminary; translation not shown

C:Accession: S25751
R:Combrinato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25751
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-231 <COM>
A:Cross-references: EMBL:X57816; NID:g33731; PIDN:CAA40953.1; PID:g33732
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:146-214/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 959; DB 2; Length 231;
Best Local Similarity 79.0%; Pred. No. 5.3e-57;
Matches 184; Conservative 14; Mismatches 23; Indels 12; Gaps 2;

QY 12 LLWLP-----GARCAYELTQPPSVSPGQTARITCGDNSRNEYVHWYQOKPAR 61
Db 1 MAWIPFLGLVAYCTGSVASYELTQPPSVSPGQTARITCGDLSGDKLGDKYASWYQOKRAGQ 60

QY 62 APILVIYDDSDRPSGIPERFSGKSGNTATLTINGVEAGDEADYYCQVMDRASDHPVFG 121
Db 61 SPVLVIYRHSKRPSGIPERFSGNSGNTATLTISGTQVMDADYYCQAWD--SSIVVEGG 118

QY 122 GTRVTVLGPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLIVLGQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

QY 182 ETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 5
S25753

Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25753
R:Combrinato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25753
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-231 <COM>
A:Cross-references: EMBL:X57818; NID:g33735; PIDN:CAA40955.1; PID:g33736
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:146-214/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 959; DB 2; Length 231;
Best Local Similarity 78.5%; Pred. No. 5.3e-57;
Matches 183; Conservative 17; Mismatches 21; Indels 12; Gaps 2;

QY 12 LLWLP-----GARCAYELTQPPSVSPGQTARITCGDNSRNEYVHWYQOKPAR 61
Db 1 MAWIPFLGLVAYCTGSVASYELTQPPSVSPGQTARITCFDGLGDKLYSSWYQOKPGQ 60

QY 62 APILVIYDDSDRPSGIPERFSGKSGNTATLTINGVEAGDEADYYCQVMDRASDHPVFG 121
Db 61 SPVLVIYQTNRPSPGIPERFSGNSGNTATLTISGTQAMDEGDYYCQAWD--SNTVVVEGG 118

QY 122 GTRVTVLGPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLIVLQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

QY 182 ETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 6.45442 Seconds

(without alignments)

1704.917 Million cell updates/sec

Title: US-09-758-173-2

Perfect score: 1243

Sequence: 1 MRVPAQLGLLLWPGARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	44.1	105	1 LAC_HUMAN	P01842 homo sapien
2	522	42.0	213	1 IL1L_HUMAN	P15814 homo sapien
3	472	38.0	111	1 LV3B_HUMAN	P80748 homo sapien
4	444	35.7	108	1 LV5A_HUMAN	P01719 homo sapien
5	417	33.5	107	1 LV4C_HUMAN	P01717 homo sapien
6	415	33.4	105	1 LAC_FIG	P01846 sus scrofa
7	412	33.1	105	1 LAC1_MOUSE	P01843 mus musculus
8	407	32.7	106	1 LV4A_HUMAN	P01715 homo sapien
9	400	32.2	111	1 LV7A_HUMAN	P01720 homo sapien
10	399	32.1	105	1 LAC_RABIT	P01847 oryctolagus
11	399	32.1	106	1 LV4B_HUMAN	P01716 homo sapien
12	397	31.9	106	1 LV4E_HUMAN	P06889 homo sapien
13	385.5	31.0	104	1 LAC1_RAT	P20766 rattus norv
14	380.5	30.6	104	1 LAC2_RAT	P20767 rattus norv
15	378	30.4	106	1 LV4D_HUMAN	P01718 homo sapien
16	377	30.3	105	1 LAC5_MOUSE	P20765 mus spretus
17	374.5	30.1	104	1 LAC3_MOUSE	P01845 mus musculus
18	369.5	29.7	104	1 LAC2_MOUSE	P01844 mus musculus
19	368	29.6	130	1 LV1G_HUMAN	P06316 homo sapien
20	360	29.0	108	1 LV3A_HUMAN	P01714 homo sapien
21	357	28.7	111	1 LV1D_HUMAN	P01702 homo sapien
22	347	27.9	105	1 LAC5_MOUSE	P20764 mus musculus
23	342	27.5	111	1 LV1C_HUMAN	P01701 homo sapien
24	331	26.6	111	1 LV6C_HUMAN	P06317 homo sapien
25	328	26.4	109	1 LV1I_HUMAN	P06888 homo sapien
26	327	26.3	111	1 LV2G_HUMAN	P01710 homo sapien
27	326.5	26.3	103	1 LAC_CHICK	P20763 gallus gall
28	326.5	26.3	112	1 LV1B_HUMAN	P01700 homo sapien
29	325.5	26.2	112	1 LV2K_HUMAN	P04209 homo sapien
30	325	26.1	111	1 LV1A_HUMAN	P01699 homo sapien
31	322.5	25.9	112	1 LV6A_HUMAN	P01721 homo sapien
32	320.5	25.8	117	1 KV1J_HUMAN	P01602 homo sapien
33	318.5	25.6	129	1 KV1W_HUMAN	P04431 homo sapien

34	318	25.6	111	1 LV2F_HUMAN	P01709 homo sapien
35	314.5	25.3	131	1 LV6E_HUMAN	P06319 homo sapien
36	313	25.2	109	1 LV1F_HUMAN	P04208 homo sapien
37	313	25.2	111	1 LV2C_HUMAN	P01706 homo sapien
38	310.5	25.0	112	1 LV1H_HUMAN	P06887 homo sapien
39	310	24.9	109	1 LV2E_HUMAN	P01708 homo sapien
40	310	24.9	111	1 LV2I_HUMAN	P01712 homo sapien
41	303	24.4	111	1 LV2A_HUMAN	P01704 homo sapien
42	302	24.3	111	1 LV2B_HUMAN	P01705 homo sapien
43	298.5	24.0	129	1 KV1X_HUMAN	P04432 homo sapien
44	298	24.0	111	1 LV2D_HUMAN	P01707 homo sapien
45	298	24.0	113	1 LV1_CHICK	P04210 gallus gall

ALIGNMENTS

RESULT 1
LAC_HUMAN STANDARD; PRT; 105 AA.

AC P01842: P80423;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain C regions.
GN IGLC1 AND IGLC2 AND IGLC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=70156723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges.";
RL J. Biol. Chem. 245:2171-2176(1970).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX MEDLINE=69088380; PubMed=4883841;
RA Milstein C., Clegg J.B., Jarvis J.M.;
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT Bence-Jones protein.";
RL Biochem. J. 110:631-652(1966).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup.";
RL J. Biochem. 93:421-429(1983).
RN [4]
RP SEQUENCE (BENCE-JONES PROTEIN KERN).
RX MEDLINE=71150336; PubMed=5549568;
RA Ponstingl H., Hess M., Hilschmann N.;
RT "Structural rule of antibodies. Primary structure of a monoclonal
RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT protein Kern). V. The complete amino acid sequence and its genetic
RT interpretation.";
RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
RN [5]
RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEMO).
RX MEDLINE=74109253; PubMed=4814727;
RA Chen B.L., Poljak R.J.;
RT "Amino acid sequence of the (lambda) light chain of a human myeloma
RT immunoglobulin (IgG New).";
RL Biochemistry 13:1295-1302(1974).
RN [6]
RP SEQUENCE (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merli G., Garver F., Ferri G.;

RT "Characterization of the two unique human anti-flavin monoclonal
 RL immunoglobulins.";
 RN Eur. J. Biochem. 228:896-893(1995).
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
 RX MEDLINE=75046825; PubMed=4215080;
 RA Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
 RT Saul F.;
 RL "The three-dimensional structure of the fab' fragment of a human
 RT myeloma immunoglobulin at 2.0-A resolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
 RN [8].
 RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
 RX MEDLINE=75013804; PubMed=4415202;
 RA Fett J.W., Deutsch H.F.;
 RT "Primary structure of the Mcg lambda chain.";
 RL Biochemistry 13:4102-4114(1974).
 RN [9].
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
 RX Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
 RA Panagiotopoulos N.;
 RT "Rotational allomerism and divergent evolution of domains in
 RT immunoglobulin light chains.";
 RL Biochemistry 14:3953-3961(1975).
 RN [10].
 RP X-RAY CRYSTALLOGRAPHY OF MCG.
 RX MEDLINE=90133913; PubMed=2515285;
 RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
 RT "Three-dimensional structure of a light chain dimer crystallized in
 RT water. Conformational flexibility of a molecule in two crystal
 RT forms.";
 RL J. Mol. Biol. 210:601-615(1989).
 RN [11].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8208680; PubMed=6273747;
 RA Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
 RT "Clustered arrangement of immunoglobulin lambda constant region genes
 RT in man.";
 RL Nature 294:536-540(1981).
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
 CC FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE
 CC KERN+ MARKER, THE NEWM PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN
 CC HAS THE KERN+ MARKER, AND THE MCG+ MARKER.
 CC -1- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
 CC 3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE
 CC (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
 CC SEQUENCE (LAMBDA-3).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; J00253; AAA59107.1; -;
 DR EMBL; L38562; AAB36581.1; ALT INIT.
 DR EMBL; X51754; CAB38569.1; ALT_INIT.
 DR EMBL; X51755; CAA36049.1; -;
 DR EMBL; X51755; CAA36051.1; -;
 DR PIR; A92057; L2HU.
 DR PDB; 2MCG; 15-JUL-92.
 DR PDB; 7FAB; 31-JAN-94.
 DR PDB; 1AOK; 04-FEB-98.
 DR PDB; 1LIL; 15-MAY-97.
 DR Genew; HGNC:5855; IGLC1.
 DR Genew; HGNC:5856; IGLC2.
 DR Genew; HGNC:5857; IGLC3.
 DR MIM; 147220; -;
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam; PFO0047; Ig; 1.
 DR SMART; SM00407; IGL1; 1.
 DR PROSITE; PS08335; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Bence-Jones protein;
 KW 3D-structure. 1 1
 FT NON_TER 1 100 IG-LIKE.
 FT DOMAIN 6 100
 FT DISULFID 27 86
 FT DISULFID 104 104
 FT VARIANT 5 5
 FT VARIANT 7 7
 FT VARIANT 45 45
 FT VARIANT 56 56
 FT VARIANT 82 82
 FT STRAND 8 11
 FT HELIX 15 19
 FT TURN 20 21
 FT STRAND 24 32
 FT STRAND 38 43
 FT TURN 44 45
 FT STRAND 46 48
 FT TURN 52 59
 FT STRAND 61 62
 FT STRAND 65 72
 FT HELIX 75 80
 FT STRAND 84 89
 FT STRAND 94 99
 SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;
 Query Match 44.1%; Score 548; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 7.6e-37;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 QPKAPSVTLFPSPSEELQANKATVCLISDFPGAVAVANKADSSPVKAGVETTPSKQ 189
 Db 1 QPKAPSVTLFPSPSEELQANKATVCLISDFPGAVAVANKADSSPVKAGVETTPSKQ 60
 QY 190 SNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 234
 Db 61 SNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 105
 RESULT 2
 ID ILL1_HUMAN STANDARD; PRT; 213 AA.
 AC P15814;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
 DE related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
 DE (CD179b antigen).
 DE IGLL1 OR IGL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89315835; PubMed=2501791;
 RA Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
 RT McKearn J.P.;
 RT "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
 RT expressed in pre-B cells and may encode the human immunoglobulin

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 22.6452 Seconds
(without alignments)
2666.544 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
Sequence: 1 MRVPAQLGLLLWLPARGC.....CQVTHGSTEKTVAPTECS 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1037	83.4	234	4 Q8N355	Q8N355 homo sapien
2	981	78.9	233	4 Q8TBC9	Q8TBC9 homo sapien
3	961	77.3	233	4 Q8N5F4	Q8N5F4 homo sapien
4	917.5	73.8	233	4 Q96169	Q96169 homo sapien
5	885	71.2	237	4 Q8WUK4	Q8WUK4 homo sapien
6	884.5	71.2	236	4 Q8NEJ1	Q8NEJ1 homo sapien
7	883	71.0	237	4 Q8WTU6	Q8WTU6 homo sapien
8	856.5	68.9	236	4 Q96E61	Q96E61 homo sapien
9	763	61.4	240	4 Q8WUK3	Q8WUK3 homo sapien
10	700	56.3	235	11 Q9NM11	Q9NM11 mus musculus
11	551	44.3	106	4 Q8TCU5	Q8TCU5 homo sapien
12	479.5	38.6	234	11 Q8VCP0	Q8VCP0 mus musculus
13	474.5	38.2	234	4 Q8NEK1	Q8NEK1 homo sapien
14	468.5	37.7	130	11 Q9D8W4	Q9D8W4 mus musculus
15	466	37.5	239	4 Q8NEK0	Q8NEK0 homo sapien
16	464	37.3	239	4 Q8TCD0	Q8TCD0 homo sapien

17	452.5	37.2	238	11 Q8VCI6	Q8VCI6 mus musculus
18	449.5	36.2	234	11 Q8R062	Q8R062 mus musculus
19	444	35.7	235	11 Q91W12	Q91W12 mus musculus
20	441.5	35.5	238	11 Q99M37	Q99M37 mus musculus
21	432.5	34.8	234	11 Q91WF8	Q91WF8 mus musculus
22	431.5	34.7	233	11 Q91WS9	Q91WS9 mus musculus
23	423	34.0	239	11 Q8VC55	Q8VC55 mus musculus
24	398.5	32.1	214	11 Q9K1A5	Q9K1A5 mus musculus
25	395.5	31.8	234	11 Q8R028	Q8R028 mus musculus
26	394	31.7	239	11 Q8K0F8	Q8K0F8 mus musculus
27	382	30.7	107	4 Q9NSD6	Q9NSD6 homo sapien
28	376.5	30.3	107	4 Q9UL82	Q9UL82 homo sapien
29	375.5	30.2	105	11 Q99JC1	Q99JC1 mus musculus
30	347	27.9	110	4 Q8T663	Q8T663 homo sapien
31	338	27.2	116	4 Q96UD0	Q96UD0 homo sapien
32	315.5	25.4	112	4 Q96JD1	Q96JD1 homo sapien
33	314	25.3	112	4 Q96JD2	Q96JD2 homo sapien
34	310	24.9	101	4 Q81ZD8	Q81ZD8 homo sapien
35	289	23.3	108	4 Q96SB0	Q96SB0 homo sapien
36	273.5	22.0	684	13 Q90544	Q90544 ginglymosto
37	264.5	21.3	127	11 Q925S9	Q925S9 mus musculus
38	260.5	21.0	112	11 Q8K1F0	Q8K1F0 mus musculus
39	252	20.3	257	13 Q90536	Q90536 ginglymosto
40	250	20.1	268	13 Q90524	Q90524 ginglymosto
41	250	20.1	471	4 Q8TC77	Q8TC77 homo sapien
42	245	19.7	106	5 Q9U410	Q9U410 schistosoma
43	244.5	19.7	112	11 Q8K1F2	Q8K1F2 mus musculus
44	244.5	19.7	134	11 Q8VDD0	Q8VDD0 mus musculus
45	244	19.6	113	11 Q8CGS1	Q8CGS1 mus musculus

ALIGNMENTS

RESULT 1

Q8N355 PRELIMINARY; PRT; 234 AA.
AC Q8N355
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028090; AAB28090.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match 83.4%; Score 1037; DB 4; Length 234;

Best Local Similarity 86.5%; Pred. No. 6.e-83;

Matches 198; Conservative 15; Mismatches 14; Indels 2; Gaps 2;

QY 7 LLGLLLWLPARGCAVELTQPPSVSVSPQOTARITCGGDSNRYVHYVHQKPARAPILV 66

Db 7 LLG-LLSHCTGSGVTSYVLTQPPSVSVAPQOTARITCGGNNAGSKSVHYVHQKPGAPVLV 65

Qy	67	IYDSDRPSGIPERFSGSKSGNTAFLTINGVEAGDEADYYCQVWDRA	SDHP -VFGGGTRV 125
Db	66	VYDSDRPSGIPERFSGSGNSGNTAFLTISRVDAGDEADYYCQLWDSSDHPVVF	GGGTKL 125
Qy	126	TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV	YAWKADSSSPVKAGVETTT 185
Db	126	TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV	YAWKADSSSPVKAGVETTT 185
Qy	186	PSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTV	APTECS 234
Db	186	PSKQSNKYAASYSLSLTPEQWKSHRSYSCQVTHGEGSTVEKTV	APTECS 234

RESULT 2

Q8TEC9	ID	Q8TEC9	PRELIMINARY;	PRT;	233 AA.
DT	01-JUN-2002	(TRENBLrel. 21, Created)			
DT	01-JUN-2002	(TRENBLrel. 21, Last sequence update)			
DT	01-MAR-2003	(TRENBLrel. 23, Last annotation update)			
DE	Hypochemical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=B-cell;				
RA	Strausberg R.;				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC022823; AAH22823.1; -				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; ig_2.				
DR	SMART; SM00406; Igv; 1.				
DR	PROSITE; PS00290; IG_MHC; 1.				
KW	Hypochemical protein.				
SQ	SEQUENCE 233 AA; 24867 MW; 367411BED6F4DF92 CRC64;				

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Query Match      78.94;  Score 981;  DB 4;  Length 233;
Best Local Similarity 79.4%;  Pred. No.5.3e-78;
Matches 185;  Conservative 17;  Mismatches 21;  Indels 10;  Gaps 1;

QY      12 LILWLP-----GARCAYELTPPPSVSVSGQTARITCGDGNRSNEYVHWYQCKPAR 61
      :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :
Db      1 MAWIFLLPLLTCTGSEASVELTPPPSVSVSGQTARITCGGDALPKQYAYWYQCKPEQ 60

QY      62 APILVIYDDSRPSPGIPERSGSKGNWALTLTNGVEAGDEADYYCQVWDRASDHVFEQG 121
      :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :
Db      61 APVLVIYKDNRPSPGIPERSGSSGTTVLTITSGVQAEDEADYYCQADSSGTYWVFGG 120

QY      122 GTRVTVLQGPRAAPSVTLPFPSSBELQANKATVLCVLSDFYPGAVTVAWKADSSPVKAGV 181
      :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :
Db      121 GTKTLTVLQGPRAAPSVTLPFPSSBELQANKATVLCVLSDFYPGAVTVAWKADSSPVKAGV 180

QY      182 ETTTPSKOSNNKYAASYSLSLTPEQWKSHRSYSCQWTHGSGTVKTVAPTCS 234
      :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :  ||| :
Db      181 ETTTPSKOSNNKYAASYSLSLTPEQWKSHKSYSCQWTHGSGTVKTVAPTCS 233

```

```

RESULT 3
QBNSF4
ID QBNSF4 PRELIMINARY; PRT; 233 AA.
AC AC
QBNSF4;
OT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT DT
OT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

```

[1]
SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032452; AAH32452.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR DR SMART; SM00409; IG; 2.
DR DR SMART; SM00407; IGC1; 1.
DR DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6AA6E3A9A CRC64;

Query Match 77.3%; Score 961; DB 4; Length 233;
Best Local Similarity 80.3%; Pred. No. 3e-76;
Matches 183; Conservative 16; Mismatches 29; Indels 0; Gaps 0

QY 7 LLGLLLLLLPLPGARCAVELTQPPSVSPGQTARITCGDGNRNEYVHWYQOKPARAPILV 56
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
6 LLPLPLTCTVSEASYELTQPPSVSPGQTARITCGDALPKKYAIWYQOKSGQTPVLV 65
QY 67 IYDDSDRSGIPERFSGSKGNTATLITNGVEAGDEADYYCYQVMDRASDPVFGGQTRVT 126
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
66 IYDDTERPGIPERFSGSSGTVATLTLGSAQVDEADYYCYSSDSSGNHWVFGGTKLT 125
QY 127 VLGGQPKAAPSVTLPSPSEELQANKATLVCLISDFYEGAVTVAAKADSSPVKAGVETTP 186
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
126 VLGGQPKAAPSVTLPFPSEEEQANKATLVCLISDFYEGAVTVAAKADSSPVKAGVETTP 185
QY 187 SKQSNKYAASYSLSLTPEQNKSHRSYSCQVTHGTSVETKTVAPTCS 234
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
186 SKQSNKYAASYSLSLTPEQNKSHRSYSCQVTHGTSVETKTVAPTCS 233

RESULT 4
Q96169 PRELIMINARY; prt; 233 AA.
ID Q96169
AC Q96169;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI TaxID=9606;

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[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-B-cell;
 RC Strausberg R.;
 RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC007782; AAH07782.1; -
 DR InterPro; IPR007110; IG-Like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR InterPro; IPR001412; tRNA_synt_I.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00178; AA.TRNA_LIGASE_I; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 SK SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;
 QW

Query Match 73.8%; Score 917.5; DB 4; Length 233;
Best Local Similarity 78.1%; Pred. NO. 1.9e-72;
Matches 178; Conservative 17; Mismatches 32; Indels 1; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:12:09 ; Search time 10.3927 Seconds
(without alignments)
952.662 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
Sequence: 1 MRVPAQLGLLLWLPARGC.....CQVTHGSTEKTVAPTECS 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243	100.0	234	3	US-08-487-550-2
2	1243	100.0	234	4	US-09-526-098-2
3	1015.5	81.7	233	3	US-08-523-894-6
4	973	78.3	236	3	US-08-487-550-10
5	973	78.3	236	4	US-09-526-098-10
6	886	71.3	234	4	US-03-372-425A-4
7	880.5	70.8	236	3	US-09-049-672A-7
8	867.5	69.8	235	3	US-09-049-672A-10
9	861	69.3	235	2	US-08-378-939-12
10	855.5	68.8	238	4	US-08-793-450-6
11	855	68.8	235	3	US-09-049-672A-12
12	844	67.9	240	3	US-09-049-672A-11
13	812	65.3	235	4	US-09-152-060-70
14	809	65.1	235	4	US-09-152-060-88
15	658.5	53.0	229	3	US-08-751-359-22
16	658.5	53.0	229	4	US-08-907-146-22
17	567	45.6	109	2	US-08-761-277A-51
18	560.5	45.1	200	6	5189147-10
19	548	44.1	105	1	US-08-422-101-9
20	548	44.1	105	1	US-08-422-091-9
21	548	44.1	105	2	US-08-422-092-9
22	548	44.1	105	2	US-08-788-800-6
23	548	44.1	105	3	US-08-422-093-9
24	548	44.1	105	3	US-08-422-112-9
25	543	43.7	106	4	US-09-313-942-14
26	535	43.0	104	4	US-09-025-769B-170
27	503	40.5	241	2	US-07-916-098A-56

28 502.5 40.4 235 3 US-08-812-586-16 Sequence 16, Appl
29 502.5 40.4 235 4 US-09-535-832A-17 Sequence 17, Appl
30 500.5 40.3 143 2 US-08-345-321-8 Sequence 8, Appl
31 500.5 40.3 236 1 US-08-157-101A-5 Sequence 5, Appl
32 496 39.9 234 4 US-09-740-002-26 Sequence 26, Appl
33 494.5 39.8 234 4 US-09-740-002-24 Sequence 24, Appl
34 492 39.6 242 4 US-09-479-614-20 Sequence 20, Appl
35 487 39.2 235 1 US-08-276-852-153 Sequence 153, App
36 487 39.2 235 1 US-08-899-575-153 Sequence 153, App
37 487 39.2 235 1 US-08-899-575-153 Sequence 153, App
38 487 39.2 235 5 PCT-US95-08743-153 Sequence 153, App
39 483.5 38.9 234 5 PCT-US94-07659-4 Sequence 4, Appl
40 477.5 38.4 234 2 US-07-690-192-2 Sequence 2, Appl
41 475 38.2 239 3 US-08-487-550-6 Sequence 6, Appl
42 475 38.2 239 4 US-09-526-098-6 Sequence 6, Appl
43 469.5 37.8 234 3 US-09-049-672A-6 Sequence 6, Appl
44 467.5 37.6 128 1 US-08-478-039-110 Sequence 110, App
45 467.5 37.6 128 1 US-08-476-349A-110 Sequence 110, App

ALIGNMENTS

RESULT 1
US-08-487-550-2
; Sequence 2, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-2

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Best Local Similarity 100.0%; Pred. No. 1.2e-102;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLGLLLWLPARGCAYELTPPSVSPQGTARITCGGDSNRYVHWYQKPA 60
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QY 61 RAPILVIYDDSDRSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
DB 61 RAPILVIYDDSDRSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
QY 121 GGTRTVLGQKAAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAG 180
DB 121 GGTRTVLGQKAAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAG 180
QY 181 VETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVKTVAPTECS 234
DB 181 VETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVKTVAPTECS 234

RESULT 2
US-09-526-098-2
; Sequence 2, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-2

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Best Local Similarity 100.0%; Pred. No. 1.2e-102;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRVPAQLGLLLWLPGARCAVELTOPPSVSPGOTARTICGGDSNRNEYVHWYQKPA 60
QY 61 RAPILVIYDDSDRSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
DB 61 RAPILVIYDDSDRSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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DB 121 GGTRTVLGQKAAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAG 180
QY 181 VETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVKTVAPTECS 234
DB 181 VETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVKTVAPTECS 234

RESULT 3
US-08-523-894-6
; Sequence 6, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-6

Query Match 81.7%; Score 1015.5; DB 3; Length 233;
Best Local Similarity 86.0%; Pred. No. 1.7e-82;
Matches 196; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

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DB 7 LLGILLWLPGARCAVELTOPPSVSPGOTARTICGGDSNRNEYVHWYQKPARAPILV 66
QY 67 IYDDSDRSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGTRV 126
DB 67 IYDDSDRSGIPERFSGSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGTRV 126
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DB 127 VLQPKAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVANKADSSPVKAGVETTP 186
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DB 187 SKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHGSGTVKTVAPTECS 234

RESULT 4
US-08-487-550-10

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 09:18:44 ; Search time 87.8457 Seconds
(without alignments)
421.442 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
Sequence: 1 MRVPAQLIGLLMLPGARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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4	1243	100.0	234	14	US-10-124-905-2
5	1015.5	81.7	233	15	US-10-211-357-6
6	1009	81.2	214	11	US-09-972-656-96
7	1001	80.5	232	12	US-10-225-108A-12
8	973	78.3	236	10	US-09-948-429B-10
9	973	78.3	236	12	US-10-124-807-10
10	973	78.3	236	12	US-10-291-532-10
11	973	78.3	236	14	US-10-124-905-10
12	944	75.9	218	11	US-09-791-153A-51
13	936.5	75.3	244	9	US-09-925-301-1424
14	932	75.0	212	11	US-09-972-656-98
15	914.5	73.6	229	12	US-10-310-719-36
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					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 6, Appl
					Sequence 96, Appl
					Sequence 12, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 51, Appl
					Sequence 1424, Ad
					Sequence 98, Appl
					Sequence 36, Appl

16	890	71.6	242	12	US-10-225-108A-14	Sequence 14, Appl
17	882	71.0	218	11	US-09-972-656-102	Sequence 102, App
18	881	70.9	234	12	US-10-194-801C-4	Sequence 4, Appl
19	880	70.8	235	10	US-09-747-669-6	Sequence 6, Appl
20	880	70.8	235	15	US-10-290-703-6	Sequence 6, Appl
21	873.5	70.3	221	14	US-10-001-857-202	Sequence 202, App
22	870.5	70.0	217	11	US-09-972-656-88	Sequence 88, Appl
23	865.5	69.6	219	10	US-09-974-443-38	Sequence 38, Appl
24	857	68.9	216	11	US-09-972-656-90	Sequence 90, Appl
25	856.5	68.9	219	15	US-10-026-925-57	Sequence 57, Appl
26	854	68.7	216	11	US-09-972-656-108	Sequence 108, App
27	816	65.6	235	12	US-10-076-747-82	Sequence 82, Appl
28	812	65.3	235	9	US-09-853-161-70	Sequence 70, Appl
29	812	65.3	235	9	US-09-852-659A-70	Sequence 70, Appl
30	812	65.3	235	10	US-09-852-797-70	Sequence 70, Appl
31	809	65.1	235	9	US-09-853-161-88	Sequence 88, Appl
32	809	65.1	235	9	US-09-852-659A-88	Sequence 88, Appl
33	809	65.1	235	10	US-09-853-797-88	Sequence 88, Appl
34	804	64.7	216	10	US-09-736-371B-19	Sequence 19, Appl
35	803.5	64.6	239	15	US-10-221-945-2	Sequence 2, Appl
36	749	60.3	239	10	US-09-828-995B-26	Sequence 26, Appl
37	746.5	60.1	246	11	US-09-909-567B-49	Sequence 49, Appl
38	691.5	55.6	216	9	US-09-291-299A-8	Sequence 8, Appl
39	665	53.5	217	9	US-09-291-299A-7	Sequence 7, Appl
40	646.5	52.0	216	9	US-09-291-299A-10	Sequence 10, Appl
41	637.5	51.3	216	9	US-09-291-299A-9	Sequence 9, Appl
42	631	50.8	139	10	US-09-796-692-901	Sequence 901, App
43	631	50.8	139	15	US-10-040-862-901	Sequence 901, App
44	626	49.6	143	10	US-09-796-692-742	Sequence 742, App
45	616	49.6	143	15	US-10-040-862-742	Sequence 742, App

ALIGNMENTS

RESULT 1
US-09-948-429B-2
Sequence 2, Application US/09948429B
Patent No. US20020177689A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSER: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09948429B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

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; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-2

Query Match          100.0%; Score 1243; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 4.8e-92;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLLGLLLMLPGARCAYELTQPPSVSPGQTARITCGGDNRSNEYVHWYQKPA 60
DB 1 MRVPAQLLGLLLMLPGARCAYELTQPPSVSPGQTARITCGGDNRSNEYVHWYQKPA 60
QY 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDPVFG 120
DB 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDPVFG 120
QY 121 GSTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
DB 121 GSTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
QY 181 VETTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 181 VETTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 2
US-10-124-807-2
; Sequence 2, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRMATIZED FORMS THEREOF,"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; City: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124.807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-807-2

Query Match          100.0%; Score 1243; DB 12; Length 234;
Best Local Similarity 100.0%; Pred. No. 4.8e-92;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLLGLLLMLPGARCAYELTQPPSVSPGQTARITCGGDNRSNEYVHWYQKPA 60
DB 1 MRVPAQLLGLLLMLPGARCAYELTQPPSVSPGQTARITCGGDNRSNEYVHWYQKPA 60
QY 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDPVFG 120
DB 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDPVFG 120
QY 121 GSTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
DB 121 GSTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
QY 181 VETTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
DB 181 VETTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 3
US-10-291-532-2
; Sequence 2, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
; APPLICANT: HARIHARAN, KANDASAMY
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/383,916
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 08/487,950
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: prmatized peptide sequence
US-10-291-532-2

Query Match          100.0%; Score 1243; DB 12; Length 234;
Best Local Similarity 100.0%; Pred. No. 4.8e-92;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRVPAQLLGLLLMLPGARCAYELTQPPSVSPGQTARITCGGDNRSNEYVHWYQKPA 60
DB 1 MRVPAQLLGLLLMLPGARCAYELTQPPSVSPGQTARITCGGDNRSNEYVHWYQKPA 60
QY 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDPVFG 120
DB 61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDPVFG 120
QY 121 GSTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
DB 121 GSTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 ; Search time 3758.85 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-3

Perfect score: 1431

Sequence: 1 ATGAACACCTGTGTTCTT.....CCCTGTCTCCGGTAATGA 1431

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1431	100.0	1431	6	AR108863	AR108863 Sequence
2	1431	100.0	1431	6	AR265197	AR265197 Sequence
3	1429.4	99.9	1431	6	BD063035	BD063035 Sequence
4	1315.8	91.9	1431	6	AR108867	AR108867 Sequence
5	1315.8	91.9	1431	6	AR265201	AR265201 Sequence
6	1314.2	91.8	1431	6	BD063039	BD063039 Sequence
7	1237.2	86.5	1431	6	EI0897	EI0897 cDNA encodl
8	1234.8	86.3	1567	6	AR135359	AR135359 Sequence
9	1227.6	85.8	1596	9	AK098516	AK098516 Homo sapi
10	1221.6	85.4	1418	6	A49389	A49389 Sequence 7
11	1215.2	84.9	1594	9	AK057754	AK057754 Homo sapi
12	1210.4	84.6	1418	6	AR176296	AR176296 Sequence
13	1209.6	84.5	1589	9	AK057775	AK057775 Homo sapi
14	1171.4	81.9	1404	6	AR135375	AR135375 Sequence
15	1170	81.8	1586	9	AK097365	AK097365 Homo sapi
16	1168.2	81.6	1404	6	AR135377	AR135377 Sequence
17	1166.6	81.5	1404	6	AR135376	AR135376 Sequence
18	1135	79.3	1428	6	BD097232	BD097232 A therape
19	1125.8	78.7	1633	9	AK097859	AK097859 Homo sapi
20	1124.2	78.6	1507	6	BD000501	BD000501 Process f
21	1123.6	78.5	1428	6	AR031184	AR031184 Sequence
22	1123.6	78.5	1428	6	AR042589	AR042589 Sequence
23	1123.6	78.5	1428	6	AR059282	AR059282 Sequence
24	1123.6	78.5	1428	6	AR076260	AR076260 Sequence
25	1123.6	78.5	1428	6	AR300617	AR300617 Sequence
26	1122.8	78.5	1425	9	AY172959	AY172959 Homo sapi
27	1122.8	78.5	1430	6	AX419496	AX419496 Sequence
28	1117.4	78.1	1679	9	BC018747	BC018747 Homo sapi
29	1117.2	78.1	1437	6	AR108865	AR108865 Sequence
30	1117.2	78.1	1437	6	AR265199	AR265199 Sequence
31	1117.2	78.1	1437	6	BD063037	BD063037 Identific
32	1116.2	78.0	1634	9	HSIG1KH	Y14735 Homo sapien
33	1115.4	77.9	1630	9	BC024289	BC024289 Homo sapi
34	1113.2	77.8	1673	9	HSIG1LH	Y14737 Homo sapien
35	1113.2	77.8	3143	9	BC019046	BC019046 Homo sapi
36	1112.4	77.7	1428	6	AR031186	AR031186 Sequence
37	1112.4	77.7	1428	6	AR042591	AR042591 Sequence
38	1112.4	77.7	1428	6	AR059284	AR059284 Sequence
39	1112.4	77.7	1428	6	AR076262	AR076262 Sequence
40	1112.4	77.7	1428	6	AR300619	AR300619 Sequence
41	1112.4	77.7	1990	9	AK098817	AK098817 Homo sapi
42	1111.6	77.7	19040	6	BD075127	BD075127 Method fo
43	1109.2	77.5	1631	9	AK097010	AK097010 Homo sapi
44	1108.4	77.5	1431	9	AY172957	AY172957 Homo sapi
45	1104.6	77.2	1465	10	S79307	S79307 Ig gamma -1

ALIGNMENTS

RESULT 1	AR108863	AR108863	Sequence 3 from patent US 6113898.	1431 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR108863	Sequence 3 from patent US 6113898.					
DEFINITION	AR108863	Sequence 3 from patent US 6113898.					
ACCESSION	AR108863	Sequence 3 from patent US 6113898.					
VERSION	AR108863.1	GI:12825139					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1431)						
AUTHORS	Anderson, D.R., Brans P., Hanna N., Shestowsky, W.S. and Heard, C.						
TITLE	Human B7.1-specific primatized antibodies and transfectomas						
JOURNAL	Patent: US 6113898-A 3 05-SEP-2000;						

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 12:12:30 ; Search time 293.094 Seconds
(without alignments)
13179.730 Million cell updates/sec

Title: US-09-758-173-3

Perfect score: 1431

Sequence: 1 ATGAACACCTGCTGCTT.....CCCTGCTCCGGTAAATGA 1431

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_15Jun03.*

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5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	18	Primates anti-hu
2	1431	100.0	1431	19	Macaque primatized
3	1431	100.0	1431	24	DNA sequence of a
4	1315.8	91.9	1431	18	Primates anti-hu
5	1315.8	91.9	1431	19	Macaque primatized
6	1315.8	91.9	1431	24	DNA sequence of a
7	1246.4	87.1	1634	21	Human immune syste
8	1237.2	86.5	1431	17	Monoclonal antibod

9	1234.8	86.3	1567	22	AAC66522	Human immune syste
10	1221.6	85.4	1418	17	AAT26889	Anti-rhesus D reco
11	1171.4	81.9	1404	18	AAT62868	Human gamma-4 heav
12	1168.2	81.6	1404	18	AAT62870	Human gamma-4PE he
13	1166.6	81.5	1404	18	AAT62869	Human gamma-4E hea
14	1135	79.3	1428	22	AAT74680	Nucleotide sequenc
15	1135	79.3	1428	25	ABT34317	Hepatitis C virus
16	1125.2	78.6	1428	18	AAT61241	Human anti-RSV mon
17	1124.2	78.6	1507	21	AAA09695	Human immunoglobul
18	1122.8	78.5	1430	24	AAK98701	CDNA of the heavy
19	1122.8	78.5	1430	25	ABX12855	Human monoclonal r
20	1117.2	78.1	1437	19	AAV35487	Macaque primatized
21	1117.2	78.1	1437	24	AAI7245	DNA sequence of a
22	1115.6	78.0	1437	18	AAT13847	Primates anti-hu
23	1115.4	77.9	1442	22	AAC84208	Plasmid Glambda-1B
24	1113.4	77.8	1798	21	AAC98220	Human colon cancer
25	1113.2	77.8	1644	22	AAS22593	Human cDNA encodin
26	1112.8	77.8	19035	19	AAV61794	Traget plasmid Man
27	1112.2	77.7	6281	22	AAC84206	Plasmid Glambda-1A
28	1110.8	77.6	1428	18	AAT61279	Human anti-RSV mon
29	1103.6	77.1	1617	14	AAQ35099	Antibody D heavy c
30	1103	77.1	1467	13	AAQ23570	Reshaped CAMPATH-1
31	1102	77.0	1599	24	ABK64550	Human benign prost
32	1102	77.0	1599	24	ABL62673	Colon adenocarcino
33	1102	77.0	1599	24	ABL65479	Lung cancer relate
34	1102	77.0	1599	24	ABL66294	Lung cancer relate
35	1100.8	76.9	1427	19	AAV41429	Plasmid Hu19Bhpcp
36	1100.8	76.9	1427	19	AAV41431	Plasmid Hu19Bhpcp
37	1098.8	76.8	1449	20	AAQ06951	Monoclonal antibod
38	1098.8	76.8	1449	20	AAQ06952	Monoclonal antibod
39	1097.6	76.7	1427	19	AAV41432	Plasmid Hu19Bhpcp
40	1096.6	76.6	1612	22	AAS22482	Human cDNA encodin
41	1096	76.6	7521	22	AAF30315	Bicistronic chimera
42	1094.2	76.5	1407	24	AAQ45757	Human C5E10 antibo
43	1094.2	76.5	1407	25	ABZ24021	Antibody C5E10 hea
44	1094	76.5	1549	13	AAQ20086	Encodes heavy chai
45	1093.8	76.4	1458	13	AAQ23571	Reshaped CD4 antib

ALIGNMENTS

RESULT 1
AAT62510
ID AAT62510 standard; DNA; 1431 BP.
XX AAT62510;
AC AAT62510;
XX 25-MAY-1997 (first entry)
DT
DE Primatized anti-human B7.1 antigen antibody 7C10 heavy chain DNA.
XX Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW primatized antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX WO9640878-A1.
PN 19-DEC-1996.
PD
XX 06-JUN-1996; 96WO-US10053.
XX 07-JUN-1995; 95US-0487550.
XX (IDEC-) IDEC PHARM CORP.
XX Anderson DR, Brams P, Hanna N, Shestowsky WS;
PI

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:05:20 ; Search time 2366.54 Seconds
(without alignments)
14696.420 Million cell updates/sec

Title: US-09-758-173-3

Perfect score: 1431

Sequence: 1 ATGAACACCTGCTGCTT.....CCCTGCTCCGGTAAATGA 1431

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first.45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_estl:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
c 1	944	66.0	1201	13	BX377695 BX377695
c 2	929.6	65.0	1142	13	BX414495 BX414495
c 3	902	63.0	1020	12	BQ062878 AGENCOURT
c 4	899.2	62.8	1045	13	BX337477 BX337477

c 5	894.8	62.5	1149	13	BX381020
c 6	892.6	62.4	1201	13	BX377803
c 7	891.2	62.3	1201	13	BX439438
c 8	889.8	62.2	902	13	BU146962
c 9	875.8	61.2	1013	13	BX360518
c 10	867.6	60.6	1200	13	BX415883
c 11	864	60.4	947	13	BQ709771
c 12	850.4	59.4	958	13	BQ706140
c 13	849.2	59.3	1093	13	BX428863
c 14	842.4	58.3	926	10	BG755166
c 15	834.2	58.3	1096	13	BX415920
c 16	831.8	58.1	1201	13	BX338493
c 17	831.2	58.1	901	12	BM007892
c 18	830.6	58.0	985	13	BX457369
c 19	830.4	58.0	988	13	BQ708857
c 20	829.4	58.0	1201	13	BX417147
c 21	824.4	57.6	1029	12	BQ063185
c 22	823.2	57.5	1019	13	BX325650
c 23	822.8	57.5	887	13	BQ711255
c 24	822.2	57.5	918	13	BQ708022
c 25	818	57.2	1015	13	BX367600
c 26	817.8	57.1	980	13	BX325701
c 27	815.2	57.0	995	12	BM914540
c 28	811.8	56.7	889	13	BX346909
c 29	811	56.7	1147	13	BX360330
c 30	809	56.5	1009	13	BX456658
c 31	808.8	56.5	881	13	BQ711291
c 32	807.4	56.4	1200	13	BX456326
c 33	804	56.2	853	13	BX388631
c 34	801.6	56.0	862	13	BX450248
c 35	800.2	55.9	1031	13	BQ064886
c 36	799.4	55.9	852	13	BX450232
c 37	798.4	55.8	1004	13	BX432300
c 38	797.4	55.7	936	13	BQ711727
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ALIGNMENTS

RESULT 1

BX377695/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1201 bp mRNA linear EST 08-MAY-2003
clone CS0DI009YJ10 3-PRIME, mRNA sequence.

GI:30439018

1 (bases 1 to 1201)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished

Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7198.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI009DE05NP1&cluster=7198.r. Contact :

Feng Liang Email: fliang@lifetech.com URL :

http://fulllength.invitrogen.com/invitroGen Corporation 1600

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Matches 991; Conservative 17; Mismatches 22; Indels 4; Gaps 4;			
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QY	578	CCAGCGGGGTGCACACCTTCCGGGTGTCCTACAGTCTCAGGACTCTACTCCCTCAGCA	637
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LOCUS			
DEFINITION			
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3-PRIME, mRNA sequence.			
ACCESSION			
BX414495			
VERSION			
BX414495.1 GI:30637021			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
1 (bases 1 to 1142)			
Li W.B., Gruber C., Jessee J. and Polayes D.			
Full-length cDNA libraries and normalization			
UNPUBLISHED			
COMMENT			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
BP 191 91006 EVRY cedex - France			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
Library was constructed by Life Technologies, a division of			
Invitrogen. This sequence belongs to sequence cluster 7198.r For			
more information about this cluster, see			
http://www.genoscope.cns.fr/			
cgi-bin/cluster.cgi?seq=CS0CAP001AE07NP1&cluster=7198.r. Contact :			
Feng Liang Email : fliang@lifetech.com URL :			
http://fulllength.invitrogen.com/Invitrogen Corporation 1600			
Faraday Avenue Genoscope sequence ID : CS0CAP001AE07NP1.			
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the Not I and EcoR V sites of the pCMVSPORT 6 vector."			
Library was not normalized."			
BASE COUNT			
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ORIGIN			
Query Match			
Best Local Similarity			
Matches 952; Conservative 6; Mismatches 9; Indels 2; Gaps 2;			
QY	463	TTCCCTCTGGCACCTCTCTCCAGAGCAGCTCTCTGGGGGACAGCGCCCTGGGTGCTG	522
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3	1315.8	91.9	1431	3	US-08-487-550-11	Sequence 11, Appl
4	1315.8	91.9	1431	4	US-09-526-098-11	Sequence 11, Appl
5	1234.8	86.3	1567	3	US-09-049-672A-17	Sequence 17, Appl
6	1210.4	84.6	1418	4	US-08-793-450-7	Sequence 7, Appli
7	1171.4	81.9	1404	3	US-08-523-894-7	Sequence 7, Appli
8	1168.2	81.6	1404	3	US-08-523-894-11	Sequence 11, Appl
9	1166.6	81.5	1404	3	US-08-523-894-9	Sequence 9, Appli
10	1123.6	78.5	1428	1	US-08-488-376-17	Sequence 17, Appl
11	1123.6	78.5	1428	2	US-08-634-223-17	Sequence 17, Appl
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14	1123.6	78.5	1428	2	US-08-635-878-17	Sequence 17, Appl
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 19:53:01 ; Search time 293.087 Seconds
(without alignments)
12894.584 Million cell updates/sec

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Gap 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1431	100.0	1431	13	US-10-124-905-3
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7	1315.8	91.9	1431	12	US-10-124-807-11
8	1315.8	91.9	1431	12	US-10-291-532-11
9	1315.8	91.9	1431	13	US-10-124-905-11
10	1314.2	91.8	1431	13	US-10-073-138-6
11	1171.4	81.9	1404	14	US-10-211-357-7
12	1168.2	81.6	1404	14	US-10-211-357-11
13	1166.6	81.5	1404	14	US-10-211-357-9
14	1135	79.3	1428	12	US-10-203-754A-40
15	1123.6	78.5	1428	9	US-09-740-002-17
16	1122.8	78.5	1430	12	US-10-225-108A-1

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Sequence 4, Appli
Sequence 230, App
Sequence 19, Appl
Sequence 15, Appl
Sequence 789, App
Sequence 1604, Ap
Sequence 445, App
Sequence 704, App
Sequence 1010, Ap
Sequence 20, Appl
Sequence 25, Appl
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Sequence 2, Appli
Sequence 27, Appl
Sequence 14, Appl
Sequence 571, App
Sequence 68, Appl
Sequence 27, Appl
Sequence 87, Appl
Sequence 111, App
Sequence 3, Appli

US-09-948-429B-3
; Sequence 3, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/948.429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,915
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

ALIGNMENTS

RESULT 1

US-09-948-429B-3
; Sequence 3, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/948.429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,915
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 55.856 Seconds
(without alignments)
1352.854 Million cell updates/sec

Title: US-09-758-173-4
Perfect score: 2577
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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2309	89.6	476	23	AAU11646
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8	2262	87.8	470	21	AAH4721
9	2230.5	86.6	475	17	AAH93553

10	2223	86.3	472	17	AAH93186
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13	2122	82.3	470	13	AAH22757
14	2112.5	82.0	467	18	AAW14927
15	2111.5	81.9	467	18	AAW14925
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17	2104.5	81.7	467	18	AAH4926
18	2104.5	81.7	581	22	AAH81972
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25	2100	81.5	451	22	AAH76948
26	2100	81.5	451	22	AAH76950
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31	2092	81.2	451	21	AAH07473
32	2092	81.2	451	22	AAH74212
33	2092	81.2	451	22	AAH76952
34	2091.5	81.2	446	17	AAH05829
35	2084.5	80.9	472	24	ABP58289
36	2079.5	80.7	475	18	AAH11639
37	2077	80.6	470	21	AAU77289
38	2073	80.4	478	19	AAH63763
39	2073	80.4	478	23	AAU11644
40	2069.5	80.3	481	13	AAH24442
41	2069	80.3	453	14	AAH33311
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ALIGNMENTS

RESULT 1

AAW01818

ID AAW01818 standard; Protein; 476 AA.

XX

AC AAW01818;

XX

DT 25-MAY-1997 (first entry)

XX

DE Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.

XX

KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;

KW primatised antibody; B7 antigen; CD28; immunosuppressive;

KW autoimmune disease; idiopathic thrombocytopenia purpura;

KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;

KW type 1 diabetes mellitus; graft versus host disease;

KW hetero-hybridoma; transfectoma.

XX

OS Chimeric Macaca cynomolgus;

OS Chimeric Homo sapiens.

XX

PN WO9640878-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US10053.

XX

PR 07-JUN-1995; 95US-0487550.

XX

PA (IDEC-) IDEC PHARM CORP.

XX

PI Anderson DR, Brans P, Hanna N, Shestowsky WS;

DR WPI: 1997-108638/10.
DR N-PSDB; AAI62510.
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
PT
PS
XX Claim 6; Fig 8B; 81pp; English.
XX
CC 2 Polypeptides (AAW01817 and AAW01819) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
CC variable genes (see also AAI62509 and AAI62510) are inserted into
CC an expression vector (pref. NIOSPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC antibodies have also been produced (see also AAW01819-22). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
SQ Sequence 476 AA;

Query Match 100.0%; Score 2577; DB 18; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.3e-146;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLVLSQVKLQWGGELLPQSETLSRTCVVSGSGISGYIYWTWIRQT 60
DB 1 MKHLWFFLLVAAPRWLVLSQVKLQWGGELLPQSETLSRTCVVSGSGISGYIYWTWIRQT 60

QY 61 PGRGLEWIGHIYNGATTNNPNSLSKSRVTISKDTSKNQFFLNLSVTDADTAVIYCARGP 120
DB 61 PGRGLEWIGHIYNGATTNNPNSLSKSRVTISKDTSKNQFFLNLSVTDADTAVIYCARGP 120

QY 121 RPDCTTTCYGGWVDWVGPDGLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 RPDCTTTCYGGWVDWVGPDGLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

QY 181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGQTQYICNVNHPKSTKV 240
DB 181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGQTQYICNVNHPKSTKV 240

QY 241 DKKAEPKCDKTHTCPCPCAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDP 300
DB 241 DKKAEPKCDKTHTCPCPCAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDP 300

QY 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

QY 361 IEKTIKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNY 420

QY 421 KTTTPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALNHYTQKSLSLSPGK 476
DB 421 KTTTPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALNHYTQKSLSLSPGK 476

RESULT 2
AAW63761
ID AAW63761 standard; Protein; 476 AA.
XX
AC AAW63761;
XX
DT 29-SEP-1998 (first entry)
XX
DE Macaque primatised 7C10 heavy chain DNA.
XX
KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;

T cell proliferation; ss.
XX
OS Macaca fascicularis.
XX
PN WO9819706-A1.
XX
PD 14-MAY-1998.
XX
XX 29-OCT-1997; 97WO-US19906.
XX
PR 08-NOV-1996; 96US-0746361.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N;
XX
XX WPI: 1998-286601/25.
DR N-PSDB; AAV35485.
XX
PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours
XX
PS Example 7; Fig 3b; 87pp; English.
XX
CC This sequence represents a primatised form of the antibody 7C10 heavy
CC chain from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC Mab can be conjugated to a drug or toxin. Mab's or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
SQ Sequence 476 AA;

Query Match 100.0%; Score 2577; DB 19; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.3e-146;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLVLSQVKLQWGGELLPQSETLSRTCVVSGSGISGYIYWTWIRQT 60
DB 1 MKHLWFFLLVAAPRWLVLSQVKLQWGGELLPQSETLSRTCVVSGSGISGYIYWTWIRQT 60

QY 61 PGRGLEWIGHIYNGATTNNPNSLSKSRVTISKDTSKNQFFLNLSVTDADTAVIYCARGP 120
DB 61 PGRGLEWIGHIYNGATTNNPNSLSKSRVTISKDTSKNQFFLNLSVTDADTAVIYCARGP 120

QY 121 RPDCTTTCYGGWVDWVGPDGLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 RPDCTTTCYGGWVDWVGPDGLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

QY 181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGQTQYICNVNHPKSTKV 240
DB 181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGQTQYICNVNHPKSTKV 240

QY 241 DKKAEPKCDKTHTCPCPCAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDP 300
DB 241 DKKAEPKCDKTHTCPCPCAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDP 300

QY 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:07:34 ; Search time 20.9182 Seconds
(without alignments)
2188.349 Million cell updates/sec

Title: US-09-758-173-4
Perfect score: 2577
Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHNYTKSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168692 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1763	68.4	330	1 GHU	Ig gamma-1 chain C
2	1626.5	63.1	377	2 A23511	Ig gamma-3 chain C
3	1624.5	63.0	377	2 A60764	Ig gamma-3 chain C
4	1600	62.1	326	1 G2HU	Ig gamma-2 chain C
5	1586.5	61.6	327	1 G4HU	Ig gamma-4 chain C
6	1537	59.6	470	2 S22080	Ig heavy chain pre
7	1525	59.2	472	2 S31459	Ig gamma-1 chain -
8	1487	57.7	374	2 S89339	Ig heavy chain v r
9	1408.5	54.7	459	2 S37483	Ig gamma-2a chain
10	1376.5	53.4	444	2 PC4436	monoclonal antibody
11	1370	53.2	446	2 S40295	Ig gamma-2a chain
12	1341	52.0	474	1 G2MS11	Ig gamma-2b chain
13	1329.5	51.6	475	2 S01321	Ig gamma-2b chain
14	1259	48.9	328	2 I47159	Ig gamma-2a chain
15	1256	48.7	255	4 S31866	Ig gamma-1 chain C
16	1253	48.6	328	2 I47160	Ig gamma-2b chain
17	1250	48.5	234	2 P70207	Ig gamma chain C r
18	1227	47.6	328	2 I47158	Ig gamma-1 chain C
19	1226.5	47.6	323	1 GHRB	Ig gamma chain C r
20	1223	47.5	328	2 I47161	Ig gamma-3 chain C
21	1212.5	47.1	329	1 G3GP	Ig gamma-2 chain C
22	1157.5	44.9	308	2 C30554	Ig heavy chain C r
23	1152	44.7	289	1 G3HUW1	Ig gamma-3 heavy C
24	1148	44.5	326	2 PS0017	Ig gamma-1 chain C
25	1142.5	44.3	333	2 PS0018	Ig gamma-2b chain C
26	1138	44.2	324	1 GIMS	Ig gamma-1 chain C
27	1137	44.1	329	1 G3MSC	Ig gamma-3 chain C
28	1133	44.0	393	1 G3MSM	Ig gamma-1 chain C
29	1126	43.7	398	1 G3MSM	Ig gamma-3 chain C

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence.revision 18-Aug-1982 #text.change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obara, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, R',98-135 <GUN>

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2

A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primärstruktur eines monoklonalen IgG1-Kammunglobulins (Myelomprotein Ni

igen Primerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nle
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q','36-96','K','98-115','Q','117-197','D','199-238','D','240','L','242-268','E','272-287','G','289-308','S','310-327','T','329-344','V'.
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R','98-197','D','199-238','E','240','M','242-266','D','268-271','D','273-330' <SOCH>
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfido bond formation in the heavy chain.
A:Reference number: A90565; MUID:71064037; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin. I. Disulfide bonds and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotrimer consists of two identical light (kappa) chains and two identical heavy (lambda) chains. In some cases, such as IgA and IgM, the subunits associate into larger oligomers. In the case of IgG, the subunits are associated into dimers by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers. In the case of IgG, the subunits are associated into dimers by interchain disulfide bonds.

C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM>
F:137-206/Domain: immunoglobulin homology <IM>
F:243-310/Domain: immunoglobulin homology <IM>
F:137-206/Domain: immunoglobulin homology <IM>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 68.4%; Score 1763; DB 1; Length 330;
Best Local Similarity 99.7%; Pred. No. 3,9e-97;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

	QY	147	ASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYEPPEPVTVSWNSGALTSGVHTFPVLQSS	206
Dd	Db	1	ASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYEPPEPVTVSWNSGALTSGVHTFPVLQSS	60
QY	207	GLXSLSVAVTPVSSLSLTQTQYICNVNKPNTKVDDKAEPKSCDKTHCTPCPAPELLGG	266	
Dd	Db	61	GLXSLSVAVTPVSSLSLTQTQYICNVNKPNTKVDDKAEPKSCDKTHCTPCPAPELLGG	120
QY	267	PSVFLPPPKPDILMISRTPEVTCCVVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPREEQYN	326	
Dd	Db	121	PSVFLPPPKPDILMISRTPEVTCCVVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPREEQYN	180
QY	327	STYRWVSVLATLVHODWLNGKEYCKVSNKALPAPIEKTIISKAKGPQRPQVYTLPSPSRDE	386	
Dd	Db	181	STYRWVSVLATLVHODWLNGKEYCKVSNKALPAPIEKTIISKAKGPQRPQVYTLPSPSRDE	240
QY	387	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	446	
Dd	Db	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	300
QY	447	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	476	
Dd	Db	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330

```

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 63.1%; Score 1626.5; DB 2; Length 377;
Best Local Similarity 81.7%; Pred. No. 5.2e-89;
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;

Qy 147 ASTKGPSVFPLAPSSKSTSGTAAALGLVVDYFPEPTVSVNSGALTSGVHTFPAVLQSS 206
Db 1 ASTKGPSVFPLAPCSRSTSGTAAALGLVVDYFPEPTVSVNSGALTSGVHTFPAVLQSS 60
Qy 207 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA----- 244
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVELKTPLDGTHTCPCRPPEKSC 120
Qy 245 -----EPKSCDKTHTCPCPAPELLGGPSVFLFPPPKDT 279
Db 121 DTPPCPCRPPEKSCDTPPCPCRPPEKSCDTPPCPCRPPELLGGPSVFLFPPPKDT 180
Qy 280 LMISRTPEVTCVVVDVSHEDPEVKFNQYVGDVEVHNNAKTPREEQYNSTYRVWSVLTVLH 339
Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNNAKTPREEQYNSTYRVWSVLTVLH 240
Qy 340 QDWLNGKEYKCKVSNKALPAPIETKISKAKGQPEQVYTLPPSRDELTKNOVSLTCLVK 399
Db 241 QDWLNGKEYKCKVSNKALPAPIETKISKAKGQPEQVYTLPPSRDEMTKNOVSLTCLVK 300
Qy 400 GFYPDSIAVESSGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSYMHE 459
Db 301 GFYPDSIAVESSGQPENNYKTTPPMLDSGDSFFLYSKLTVDKSRWQQGNVFCSYMHE 360
Qy 460 ALHNHYTKQSLSLSPGK 476
Db 361 ALHNRYTKQSLSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 con
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

```

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Emb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 13.1295 Seconds
(without alignments)
1704.917 Million cell updates/sec

Title: US-09-758-173-4
Perfect score: 2577
Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHNHYTKSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	68.4	330	GCL_HUMAN	P01857 homo sapien
2	1600	62.1	326	GCL_HUMAN	P01859 homo sapien
3	1586.5	61.6	327	GCL_HUMAN	P01861 homo sapien
4	1226.5	47.6	323	GC_RABIT	P01870 oryctolagus
5	1212.5	47.1	329	GC2_CAVPO	P01862 cavia porce
6	1157	44.9	320	GCL_HUMAN	P01860 homo sapien
7	1148	44.5	326	GCL_RAT	P20759 rattus norv
8	1142.5	44.3	333	GCB_RAT	P20761 rattus norv
9	1138	44.2	324	GCL_MOUSE	P01868 mus musculu
10	1137	44.1	329	GCL_MOUSE	P22436 mus musculu
11	1133	44.0	393	GCL_MOUSE	P01869 mus musculu
12	1126	43.7	398	GCL_MOUSE	P03987 mus musculu
13	1122	43.5	330	GCA_MOUSE	P01863 mus musculu
14	1119.5	43.4	335	GCA_MOUSE	P01864 mus musculu
15	1117	43.3	399	GCA_MOUSE	P01865 mus musculu
16	1114.5	43.2	329	GCL_RAT	P20762 rattus norv
17	1108	43.0	322	GCA_RAT	P20760 rattus norv
18	1085	42.1	336	GCB_MOUSE	P01866 mus musculu
19	1080	41.9	405	GCB_MOUSE	P01867 mus musculu
20	489	19.0	428	EPC_HUMAN	P01854 homo sapien
21	483.5	18.8	429	EPC_RAT	P01855 rattus norv
22	468	18.2	146	HV2I_HUMAN	P06331 homo sapien
23	465	18.0	421	EPC_MOUSE	P06336 mus musculu
24	442	17.2	454	GCL_HUMAN	P01871 homo sapien
25	441.5	17.1	455	MUC_MOUSE	P01872 mus musculu
26	437	17.0	458	MUC_RABIT	P03988 oryctolagus
27	431.5	16.7	476	MUC_MOUSE	P01873 mus musculu
28	427	16.6	479	MUC_RABIT	P04221 oryctolagus
29	425	16.5	457	MUC_SUNMU	P20768 suncus muri
30	420	16.3	450	MUC_CANFA	P01874 canis famil
31	415.5	16.1	454	MUC_MESAU	P06337 mesocricetu
32	403	15.6	391	MUCB_HUMAN	P04220 homo sapien
33	394	15.3	438	HVCS_HETER	P23087 heterodontu

ALIGNMENTS

RESULT 1

ID	GCL_HUMAN	STANDARD	PRT	330 AA
AC	P01857			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RL	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RL	chymotryptic peptides of the H-chain, alignment of the tryptic			
RL	peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

34	330.5	15.2	370	1	HVC1_HETER	P23084 heterodontu
35	386.5	15.0	438	1	HVC2_HETER	P23085 heterodontu
36	385	14.9	461	1	HVCM_HETER	P23086 heterodontu
37	383.5	14.9	353	1	ALC1_HUMAN	P01876 homo sapien
38	380.5	14.8	353	1	ALC1_GORGO	P20758 gorilla gor
39	379	14.7	340	1	ALC2_HUMAN	P01877 homo sapien
40	371	14.4	129	1	HV2F_HUMAN	P01824 homo sapien
41	362.5	14.1	393	1	HVC3_HETER	P23086 heterodontu
42	361	14.0	117	1	HV2G_HUMAN	P01825 homo sapien
43	356.5	13.8	137	1	HV46_MOUSE	P01822 mus musculu
44	355	13.6	116	1	HV60_MOUSE	P18531 mus musculu
45	344	13.3	344	1	ALC_MOUSE	P01878 mus musculu

RT Intrachain disulfide bonds.;
 RL Biochemistry 9:3188-3196(1970).
 [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Preker L., Schwarz J., Reichel W., Hilschmann N.;
 RT Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein NIE), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.;
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 [8]
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RP MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RL aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35-116, 198, 269 & 272.
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 156, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198, 267 & 272.
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 CC -----
 CC EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A93433; GHU.
 DR PDB: 1FC1; 15-JUL-92.
 DR PDB: 1FC2; 15-JUL-92.
 DR PDB: 1AJ7; 12-NOV-97.
 DR PDB: 1D3B; 09-FEB-00.
 DR PDB: 1D51; 09-FEB-00.
 DR PDB: 1D6V; 04-OCT-00.
 DR PDB: 1DN2; 17-MAY-00.
 DR PDB: 1E4K; 06-JUN-01.
 DR PDB: 1FCC; 20-JUL-95.
 DR PDB: 1H2H; 12-JUN-02.
 DR PDB: 1I7Z; 08-AUG-01.
 DR PDB: 1IIS; 16-MAY-01.
 DR PDB: 1IIX; 16-MAY-01.
 DR PDB: 1L6X; 10-APR-02.
 DR PDB: 2RGS; 12-NOV-97.
 DR Genew: HGNC:5525; IGHG1.
 DR MIM: 147100;
 DR GO: GO:0005624; C-membrane fraction; NAS.
 DR GO: GO:0003823; F-antigen binding activity; TAS.
 DR GO: GO:0008955; P-immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; IGH1; 2.
 DR PROSITE: PS00835; IG_LIKE; 3.
 DR PROSITE: PS00230; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 3D-structure. 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330
 FT DISULFID 27 83
 FT DISULFID 103 103
 FT DISULFID 109 109
 FT DISULFID 112 112
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 122 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 147
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 166
 FT TURN 168 171
 FT STRAND 176 179
 FT TURN 180 181
 FT STRAND 182 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT STRAND 238 242
 FT STRAND 245 256
 FT STRAND 260 265
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 305 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 325
 SQ SEQUENCE 330 AA; 36106 MW; 3770E106C2FA33D CRC64;
 Query Match 68.4%; Score 1763; DB 1; Length 330;
 Best Local Similarity 99.7%; Pred. No. 2.3e-117; Indels 0; Gaps 0;
 Matches 329; Conservative 0; Mismatches 1;
 QY 147 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
 DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 207 GLYSLSVVTVPPSSSLGTQTVICNVNHPKNTKVKKAEPKSCDKTHTCPPCPAPPELLGG 266
 DB 61 GLYSLSVVTVPPSSSLGTQTVICNVNHPKNTKVKKAEPKSCDKTHTCPPCPAPPELLGG 120
 QY 267 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 326
 DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180
 QY 327 STYRVSVLTIVLHODWLNKGYCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDE 386
 DB 181 STYRVSVLTIVLHODWLNKGYCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDE 240
 QY 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 446
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 46.0645 Seconds
(without alignments)
2666.544 Million cell updates/sec

Title: US-09-758-173-4
Perfect score: 2577
Sequence: 1 MKHLWFLVLAAPRWLSQ.....MHEALNHVTKSLSPCK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_page.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2041.5	79.2	471	Q8TC77	Q8TC77 homo sapien
2	2017	78.3	473	Q8TC63	Q8TC63 homo sapien
3	1884.5	73.1	521	Q8N4Y9	Q8N4Y9 homo sapien
4	1614	62.6	509	Q8NF17	Q8NF17 homo sapien
5	1429	55.5	469	Q8R3V9	Q8R3V9 mus musculus
6	1423.5	55.2	463	Q91LC4	Q91LC4 mus musculus
7	1405	54.5	468	Q91L31	Q91L31 mus musculus
8	1403.5	54.5	473	Q9D814	Q9D814 mus musculus
9	1389.5	53.9	437	Q9R1A4	Q9R1A4 mus musculus
10	1383.5	53.7	473	Q91L25	Q91L25 mus musculus
11	1333.5	51.7	473	Q91Z05	Q91Z05 mus musculus
12	1325	51.4	474	Q8R3H6	Q8R3H6 mus musculus
13	1268	49.2	701	Q96PQ8	Q96PQ8 homo sapien
14	1262.5	49.0	337	Q95M34	Q95M34 equus caball
15	950.5	36.9	597	Q9BU10	Q9BU10 homo sapien
16	948.5	36.8	597	Q9BQB8	Q9BQB8 homo sapien

17	940.5	36.5	588	4	Q8WUX4	Q8WUX4 homo sapien
18	940.5	36.5	613	4	Q96AA6	Q96AA6 homo sapien
19	931	36.1	613	4	Q96EY0	Q96EY0 homo sapien
20	856	33.2	496	4	Q96KX8	Q96KX8 homo sapien
21	745.5	28.9	597	4	Q96BB9	Q96BB9 homo sapien
22	727.5	28.2	479	11	Q99M22	Q99M22 mus musculus
23	719	27.9	613	11	Q8VCX7	Q8VCX7 mus musculus
24	718	27.9	613	4	Q8WUK1	Q8WUK1 homo sapien
25	712	27.6	278	11	Q921K1	Q921K1 mus musculus
26	693.5	26.9	499	4	Q8N5K4	Q8N5K4 homo sapien
27	691.5	26.8	614	4	Q96GA6	Q96GA6 homo sapien
28	688	26.7	482	11	Q91X92	Q91X92 mus musculus
29	665	25.8	494	4	Q96K68	Q96K68 homo sapien
30	654.5	25.4	493	4	Q8NCL6	Q8NCL6 homo sapien
31	651	25.3	496	4	Q96DK0	Q96DK0 homo sapien
32	640	24.8	500	4	Q9BRV0	Q9BRV0 homo sapien
33	632	24.5	488	11	Q91WR1	Q91WR1 mus musculus
34	631.5	24.5	487	11	Q99KA4	Q99KA4 mus musculus
35	630.5	24.5	497	4	Q8WY24	Q8WY24 homo sapien
36	629.5	24.4	481	11	Q91WT1	Q91WT1 mus musculus
37	625	24.3	486	11	Q91Z07	Q91Z07 mus musculus
38	621.5	24.1	481	11	Q8VCV5	Q8VCV5 mus musculus
39	620.5	24.1	479	11	Q91WP5	Q91WP5 mus musculus
40	618.5	24.0	484	11	Q8VEA0	Q8VEA0 mus musculus
41	617.5	24.0	480	11	Q91XE1	Q91XE1 mus musculus
42	616	23.9	482	11	Q8KI72	Q8KI72 mus musculus
43	612	23.7	488	11	Q8KOF2	Q8KOF2 mus musculus
44	607.5	23.6	481	11	Q91WT3	Q91WT3 mus musculus
45	600.5	23.3	489	11	Q8VCX4	Q8VCX4 mus musculus

ALIGNMENTS

RESULT 1	Q8TC77	PRELIMINARY;	PRT;	471 AA.
Q8TC77	AC	Q8TC77:		
DT	01-JUN-2002	(TRENBLrel. 21, Created)		
DT	01-JUN-2002	(TRENBLrel. 21, Last sequence update)		
DT	01-MAR-2003	(TRENBLrel. 23, Last annotation update)		
DE		Hypothetical protein.		
OS		Homo sapiens (Human).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX		NCBI_TaxID=9606;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=Splicein;		
RA		Strausberg R.;		
RL		Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL	BC024289; AAH24289.1; -		
DR	InterPro	IPR007110; IG-like.		
DR	InterPro	IPR003006; IG_MHC.		
DR	InterPro	IPR003596; IG_v.		
DR	Pfam	PF00047; ig_4.		
DR	SMART	SM00406; IGV. 1.		
DR	PROSITE	PS50835; IG-LIKE; 4.		
DR	PROSITE	PS00290; IG_MHC; 2.		
KW		Hypothetical protein.		
SQ		SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;		
		Query Match 79.2%; Score 2041.5; DB 4; Length 471;		
		Best Local Similarity 82.8%; Pred. No. 1.7e-164;		
		Matches 391; Conservative 22; Mismatches 52; Indels 7; Gaps 4;		
QY	5	WFFLLVLAAPRWVLSQVKLQWGGGLLPSETLRSPTCVSGSGSYGYVYTWTRQTPGRG	64	
DB	7	WYF--LVAILGVQCEVOLVSGGGLVKGSGLSLCAASGFTFS--YSNNWVRQAPGK	63	
QY	65	LEWIGHYNGGATNPNPNSLRVTSKDTSKNOFFFLNLSVTDADTAVTYCARGPRPDC	124	
DB	64	LEWVSSMSSSSSIYIYADSVKRGFTISRDNKNSLYLQMNELRAEDTAVTYCARDLR-QL	122	

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QY 125 TTICYGWVDWVGPDLLVTVSSASTKQPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV 184
D 123 TSWT--FDLWGRGLTVVSSASTKQPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV 179
QY 185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSTLGTQTYICNVNHNKPSNTKYDKKA 244
D 180 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSTLGTQTYICNVNHNKPSNTKYDKKV 239
QY 245 EFKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 304
D 240 EFKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 299
QY 305 NNYVDGVEVHNAKTPREQYNSTYRVVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKT 364
D 300 NNYVDGVEVHNAKTPREQYNSTYRVVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKT 359
QY 365 ISKAGQPREPOVYITLPSRDELTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNYKTTTP 424
D 360 ISKAGQPREPOVYITLPSRDELTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNYKTTTP 419
QY 425 PVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
D 420 PVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 471

RESULT 2
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueCL1.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; Igv. 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match
Best Local Similarity 78.3%; Score 2017; DB 4; Length 473;
Matches 388; Conservative 29; Mismatches 48; Indels 12; Gaps 4;

QY 1 MKHLWFFLLVAAAPRWLVSVQVLLQWEGELLPSETLISRCVVGSGSI-SGYIYTWIRQ 59
D 8 MKHLWFFLLVAAAPRWLVSVQVLLQWEGELLPSETLISRCVVGSGSI-SGYIYTWIRQ 67
QY 60 TFGRLGIEWTGHYGNAGATNPNPSLKSRTISKDTSKNQFFLNLSVTDADTAVYICARG 119
D 68 PPKGGLIEWTGHYGNAGATNPNPSLKSRTISKDTSKNQFFLNLSVTDADTAVYICARG 126
QY 120 PRDCTTCYCGWVDWVGPDLLVTVSSASTKQPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
D 127 H-----LVMGFGAHWGQGLVSVSPASTKQPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
QY 180 PEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSTLGTQTYICNVNHNKPSNTK 239
```

```
DB 180 PEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSTLGTQTYICNVNHNKPSNTK 239
QY 240 VDKKAEKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 299
D 240 VDKKAEKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 296
QY 300 PEVFNKYGVEVHNAKTPREQYNSTYRVVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKT 359
D 297 PEVFNKYGVEVHNAKTPREQYNSTYRVVSVLTVLHQDLNMGKEYCKKVSNNKALPAPIEKT 356
QY 360 PIEKTIKAKQPREPOVYITLPSRDELTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNY 419
D 357 SIEKTIKAKQPREPOVYITLPSRDELTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNY 416
QY 420 YKTPPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
D 417 YKTPPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 3
Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match
Best Local Similarity 73.1%; Score 1884.5; DB 4; Length 521;
Matches 368; Conservative 32; Mismatches 61; Indels 63; Gaps 5;

QY 7 FLLVAAAPRWLVSVQVLLQWEGELLPSETLISRCVVGSGSI-SGYIYTWIRQTPGRL 66
D 7 WLLVVFLLQVQCEVQLVDSGGGLVQPGSLRLSCAASGFIIVSDHYV-ENVQAPQKGP 65
QY 67 WIG--HIYGNAGATNPNPSLKSRTISKDTSKNQFFLNLSVTDADTAVYICAR----G 119
D 66 WVGCFRKAHSTTEYAASVKGRTILRDSKSVHLQNNSLATDDTAVYICVVDLEGAG 125
QY 120 PRDCTTCYCGWVDWVGPDLLVTVSSASTKQPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
D 126 K-----YDWFYDIWGRGLVTVSSASTKQPSVFPLAPSSKSTSGGTAALGCLVKDYF 177
QY 180 PEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSTLGTQTYICNVNHNKPSNTK 239
D 178 PEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSTLGTQTYICNVNHNKPSNTK 237
QY 240 VDKKA-----EPKSCDKT 252
D 238 VDKRVELKTPGLDTHTCRCRPEPKSCDTPPPPCRCPEPKSCDTP 297
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:12:09 ; Search time 21.1407 seconds
(without alignments)
952.662 Million cell updates/sec

Title: us-09-758-173-4

Perfect score: 2577

Sequence: 1 MKHLFFLLVAAPRWLSQ.....MHEALHNYTKLSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pap.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pap.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pap.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pap.*
- 5: /cgn2_6/prodata/1/iaa/PCUS_COMB.pap.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2577	100.0	476	3	US-08-487-550-4
2	2577	100.0	476	4	US-09-526-098-4
3	2309	89.6	476	3	US-08-487-550-12
4	2309	89.6	476	4	US-09-526-098-12
5	2277.5	88.4	473	3	US-09-049-672A-4
6	2206	85.6	472	4	US-08-793-450-8
7	2112.5	82.0	467	3	US-08-523-894-12
8	2111.5	81.9	467	3	US-08-523-894-8
9	2106.5	81.7	466	3	US-08-397-411-7
10	2104.5	81.7	467	3	US-08-523-894-10
11	2100	81.5	451	2	US-08-887-352B-14
12	2100	81.5	451	2	US-08-887-352B-16
13	2100	81.5	451	3	US-08-466-151-65
14	2100	81.5	451	3	US-09-109-207C-14
15	2100	81.5	451	3	US-09-109-207C-16
16	2100	81.5	451	3	US-09-296-005-14
17	2100	81.5	451	3	US-09-296-005-16
18	2092	81.2	451	2	US-08-887-352B-18
19	2092	81.2	451	3	US-09-109-207C-18
20	2092	81.2	451	3	US-09-282-505-2
21	2092	81.2	451	3	US-09-054-255-2
22	2092	81.2	451	3	US-09-296-005-18
23	2092	81.2	451	4	US-09-282-846-2
24	2092	81.2	451	4	US-09-680-145-2
25	2075.5	80.5	475	4	US-09-740-002-25
26	2073	80.4	478	3	US-08-487-550-8
27	2073	80.4	478	4	US-09-526-098-8

28	2069	80.3	453	3	US-08-466-151-8	Sequence 8, Appl
29	2069	80.3	453	4	US-08-466-163B-8	Sequence 8, Appl
30	2061.5	80.0	452	3	US-09-027-449-71	Sequence 71, Appl
31	2061.5	80.0	452	3	US-09-026-985-71	Sequence 71, Appl
32	2061.5	80.0	452	4	US-09-121-952A-71	Sequence 71, Appl
33	2061.5	80.0	452	4	US-09-234-340A-71	Sequence 71, Appl
34	2047.5	79.5	475	4	US-09-740-002-27	Sequence 27, Appl
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36	2032.5	78.9	449	4	US-09-679-397-2	Sequence 2, Appl
37	2032.5	78.9	449	4	US-09-680-148-2	Sequence 2, Appl
38	2032.5	78.9	449	4	US-09-304-465A-2	Sequence 2, Appl
39	2025	78.6	449	1	US-08-458-516-13	Sequence 13, Appl
40	2019.5	78.4	462	4	US-09-289-942A-7	Sequence 7, Appl
41	2003.5	77.7	459	1	US-08-157-101A-7	Sequence 7, Appl
42	1998	77.5	472	4	US-09-301-593-30	Sequence 30, Appl
43	1997.5	77.5	467	3	US-09-049-672A-8	Sequence 8, Appl
44	1978	76.8	472	4	US-09-301-593-43	Sequence 43, Appl
45	1976.5	76.7	453	4	US-09-301-593-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-4
; Sequence 4, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-4

Query Match 100.0%; Score 2577; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.6e-206;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAHLFFLLVAAPRWLSQVKLQGWEGGLQPSLRSCTCVYSGGSGISGYYWTWIRQT 60
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DB 121 RPDCTTICYGWVDVWVGDLVTVSSASTKGPSVFPLAPSSKSGSTAALGCLVKDYFP 180
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DB 181 EPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKV 240
QY 241 DKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDP 300
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DB 301 EVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
QY 361 IEKTSKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDSIAVENESGQPENNY 420
DB 361 IEKTSKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDSIAVENESGQPENNY 420
QY 421 KTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCVMEALHNHYTQKSLSLSPGK 476
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RESULT 2
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; Sequence 4, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/526,098
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 09/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-526-098-4
Query Match 100.0%; Score 2577; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.6e-206;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 PGRLEWIGHYNGATTINPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVVYCARGP 120
QY 121 RPDCTTICYGWVDVWVGDLVTVSSASTKGPSVFPLAPSSKSGSTAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVWVGDLVTVSSASTKGPSVFPLAPSSKSGSTAALGCLVKDYFP 180
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QY 241 DKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDP 300
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DB 361 IEKTSKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDSIAVENESGQPENNY 420
QY 421 KTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCVMEALHNHYTQKSLSLSPGK 476
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RESULT 3
US-09-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/487,550
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:18:44 ; Search time 178.695 Seconds
(without alignments)
421.442 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA:*

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- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2577	100.0	476	12	Sequence 4, Appl
3	2577	100.0	476	12	Sequence 4, Appl
4	2577	100.0	476	12	Sequence 4, Appl
5	2309	89.6	476	14	US-10-124-905-4
6	2309	89.6	476	12	US-09-948-429B-12
7	2309	89.6	476	12	US-10-124-807-12
8	2309	89.6	476	12	US-10-291-532-12
9	2112.5	82.0	467	15	US-10-124-905-12
10	2111.5	81.9	467	15	US-10-211-357-12
11	2104.5	81.7	467	15	US-10-211-357-8
12	2103	81.6	451	11	US-10-211-357-10
13	2100	81.5	451	9	US-09-925-179-66
14	2100	81.5	451	9	US-09-920-171-14
15	2100	81.5	451	11	US-09-925-179-65

16	2100	81.5	451	12	US-10-113-996-14
17	2100	81.5	451	12	US-10-113-996-16
18	2099	81.5	451	11	US-09-925-179-68
19	2092	81.2	451	9	US-09-920-171-18
20	2092	81.2	451	12	US-10-113-996-18
21	2092	81.2	451	12	US-10-292-869-2
22	2092	81.2	451	12	US-09-792-938-2
23	2075.5	80.5	475	9	US-09-740-002-25
24	2073	80.4	478	10	US-09-948-429B-8
25	2073	80.4	478	12	US-10-124-807-8
26	2073	80.4	478	12	US-10-291-532-8
27	2073	80.4	478	14	US-10-124-905-8
28	2069	80.3	453	9	US-09-802-077-8
29	2069	80.3	453	9	US-09-802-079-8
30	2069	80.3	453	11	US-09-925-196-8
31	2061.5	80.0	452	11	US-09-726-258-71
32	2055	79.7	580	12	US-10-310-719-37
33	2053.5	79.7	467	15	US-10-171-452A-41
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36	2050.5	79.6	467	15	US-10-171-452A-53
37	2047.5	79.5	475	9	US-09-740-002-27
38	2047	79.4	451	10	US-09-996-288-230
39	2047	79.4	451	11	US-09-996-265-230
40	2046	79.4	474	12	US-10-325-108A-3
41	2046	79.4	474	12	US-09-848-832-3
42	2045.5	79.4	450	9	US-09-796-848A-43
43	2045.5	79.4	450	9	US-09-796-848A-49
44	2045.5	79.4	450	10	US-09-996-288-216
45	2045.5	79.4	450	10	US-09-996-288-218

ALIGNMENTS

RESULT 1
US-09-948-429B-4
; Sequence 4, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948.429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620

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; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-4

Query Match      100.0%; Score 2577; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.8e-179;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKHLWFFLLVAAPRWLSQVKLQGWGEGLLQPSSETLSRVCVYSGGSGISGYYTWTWIRT 60
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DB 61 PGRGLEWIGHYNGGATTNPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARGP 120
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DB 121 RPDCTTICYGWVDVWPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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DB 301 EVKFNWYVDGVEVHNKATKPREEQNSTYRYVSVTLVHODWLNKGEYKCKVSNKALPAP 360
QY 361 IEKTSKAGKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTSKAGKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTPLVDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DB 421 KTTPLVDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 2
US-10-124-807-4
; Sequence 4, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124.807
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-807-4

Query Match      100.0%; Score 2577; DB 12; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.8e-179;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKHLWFFLLVAAPRWLSQVKLQGWGEGLLQPSSETLSRVCVYSGGSGISGYYTWTWIRT 60
QY 61 PGRGLEWIGHYNGGATTNPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARGP 120
DB 61 PGRGLEWIGHYNGGATTNPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARGP 120
QY 121 RPDCTTICYGWVDVWPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVWPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 181 EPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSN TKV 240
DB 181 EPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSN TKV 240
QY 241 DKAAPKSKCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
DB 241 DKAAPKSKCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNKATKPREEQNSTYRYVSVTLVHODWLNKGEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNKATKPREEQNSTYRYVSVTLVHODWLNKGEYKCKVSNKALPAP 360
QY 361 IEKTSKAGKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTSKAGKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTPLVDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DB 421 KTTPLVDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 3
US-10-291-532-4
; Sequence 4, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 ; Search time 1891.24 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-5
Perfect score: 720
Sequence: 1 ARGAGCCCTCCCTGCTCAGCT.....TCAACAGGGGAGAGCTTTGA 720

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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GenEmbl.*

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10: gb_ro.*
11: gb_sts.*
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13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
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19: em_mu.*
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24: em_ph.*
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26: em_ro.*
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28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	720	100.0	720	6	AR108864	AR108864 Sequence
2	720	100.0	720	6	AR265198	AR265198 Sequence
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4	628.4	87.3	973	9	BC022362	BC022362 Homo sapi
5	622	86.4	720	6	E40698	E40698 Antihuman F
6	620.4	86.2	891	6	E40748	E40748 Antihuman F
7	618.8	85.9	720	6	E40696	E40696 Antihuman F
8	618.8	85.9	720	6	E40697	E40697 Antihuman F
9	617.2	85.7	720	6	E40695	E40695 Antihuman F
10	607.6	84.4	972	9	BC030814	BC030814 Homo sapi
11	606	84.2	1081	6	AX540421	AX540421 Sequence
12	601.2	83.5	963	6	AX067347	AX067347 Sequence
13	599.6	83.3	830	9	AB064106	AB064106 Homo sapi
14	599.4	83.2	720	6	E35205	E35205 Human monon
15	599.4	83.2	720	6	E35207	E35207 Human monon
16	598.8	83.2	720	6	E35208	E35208 Human monon
17	598.2	83.1	720	6	E35204	E35204 Human monon
18	598	83.1	830	9	AB064102	AB064102 Homo sapi
19	596.6	82.9	720	6	E35201	E35201 Human monon
20	595.4	82.7	720	6	E35206	E35206 Human monon
21	593.4	82.4	720	6	E35203	E35203 Human monon
22	591.6	82.2	720	6	E35202	E35202 Human monon
23	591.4	82.1	977	9	BC034142	BC034142 Homo sapi
24	588.4	81.7	944	9	AK096938	AK096938 Homo sapi
25	588.4	81.7	968	6	AX616323	AX616323 Sequence
26	587.8	81.6	720	6	E35209	E35209 Human monon
27	587.8	81.6	720	6	E35210	E35210 Human monon
28	583.4	81.0	786	9	AB064059	AB064059 Homo sapi
29	580.4	80.6	794	9	AB064137	AB064137 Homo sapi
30	578.8	80.4	775	9	AB064133	AB064133 Homo sapi
31	578.8	80.4	829	9	AB064101	AB064101 Homo sapi
32	572.4	79.5	857	9	AB064090	AB064090 Homo sapi
33	570.8	79.3	786	9	AB064057	AB064057 Homo sapi
34	569.2	79.1	794	9	AB064136	AB064136 Homo sapi
35	566	78.6	791	9	AB064135	AB064135 Homo sapi
36	566	78.6	827	9	AB064105	AB064105 Homo sapi
37	566	78.6	828	9	AB064104	AB064104 Homo sapi
38	564.4	78.4	783	9	AB064054	AB064054 Homo sapi
39	561.2	77.9	726	6	E10698	E10698 cDNA encodi
40	561.2	77.9	785	9	AB064055	AB064055 Homo sapi
41	556.4	77.3	784	9	AB064058	AB064058 Homo sapi
42	556.4	77.3	829	9	AB064112	AB064112 Homo sapi
43	554.8	77.1	857	9	AB064092	AB064092 Homo sapi
44	554.8	77.1	858	9	AB064091	AB064091 Homo sapi
45	554.8	77.1	858	9	AB064093	AB064093 Homo sapi

ALIGNMENTS

RESULT 1
AR108864
LOCUS AR108864
DEFINITION Sequence 5 from patent US 6113898.
ACCESSION AR108864
VERSION AR108864.1 GI:12925140
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 720)
AUTHORS Anderson,D.R., Brans,P., Hanna,N., Shestovsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
JOURNAL Patent: US 6113898-A 5 05-SEP-2000;

DNA linear PAT 14-FEB-2001

FEATURES		Location/Qualifiers		Location/Qualifiers	
source		1..720		1..720	
BASE COUNT		178 a 200 c 193 g		178 a 200 c 193 g	
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Query Match		100.0%; Score 720; DB 6; Length 720;			
Best Local Similarity		100.0%; Pred. No. 1.6e-194;			
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG	60		
DB	1	ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG	60		
QY	61	GAAGTTGTGATGACTCAGCTCCTCCACTGTCCCTTCCCATCACACTGGAGAGCGGCTCC	120		
DB	61	GAAGTTGTGATGACTCAGCTCCTCCACTGTCCCTTCCCATCACACTGGAGAGCGGCTCC	120		
QY	121	ATCTCCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCTGTAGTTGG	180		
DB	121	ATCTCCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCTGTAGTTGG	180		
QY	181	TATCAGCAGAGCCAGGCGCAACCTCCCAAGCTCCTGATTTATAGGTTTCTAACCGGGAC	240		
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QY	241	TCTGGGGTCCAGACAGATTTCAGGGCAGTGGGGCAGGACAGATTTCACACTGAAATTC	300		
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QY	301	AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAAGGACTCCT	360		
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QY	361	CCCACTTTCCGGGAGGAGGACCAAGTGGAAATCAACAGTACGTTGGCTGCACCATCTGTC	420		
DB	361	CCCACTTTCCGGGAGGAGGACCAAGTGGAAATCAACAGTACGTTGGCTGCACCATCTGTC	420		
QY	421	TTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGTTGTGCTCGCTG	480		
DB	421	TTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGTTGTGCTCGCTG	480		
QY	481	CTGAATACTTCTATCCAGAGAGGCCAAGTACAGTGGAGTGGATACGCCCTCCAA	540		
DB	481	CTGAATACTTCTATCCAGAGAGGCCAAGTACAGTGGAGTGGATACGCCCTCCAA	540		
QY	541	TCGGTTAACTCCAGAGAGTGTCCACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC	600		
DB	541	TCGGTTAACTCCAGAGAGTGTCCACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC	600		
QY	601	AGCAGCACCCCTGACCTCAGCAAGGACAGCTACGAGAAACACAAAGTCTACGGCTCGAA	660		
DB	601	AGCAGCACCCCTGACCTCAGCAAGGACAGCTACGAGAAACACAAAGTCTACGGCTCGAA	660		
QY	661	GTACCCATCAGGGCTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGTGA	720		
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LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
1 (bases 1 to 720)					
AUTHORS					
Anderson, D.R., Hanna, N., Brans, P. and Hard, C.					

FEATURES		Location/Qualifiers		Location/Qualifiers	
source		1..720		1..720	
BASE COUNT		178 a 200 c 193 g		178 a 200 c 193 g	
ORIGIN					
Query Match		100.0%; Score 720; DB 6; Length 720;			
Best Local Similarity		100.0%; Pred. No. 1.6e-194;			
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG	60		
DB	1	ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG	60		
QY	61	GAAGTTGTGATGACTCAGCTCCTCCACTGTCCCTTCCCATCACACTGGAGAGCGGCTCC	120		
DB	61	GAAGTTGTGATGACTCAGCTCCTCCACTGTCCCTTCCCATCACACTGGAGAGCGGCTCC	120		
QY	121	ATCTCCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCTGTAGTTGG	180		
DB	121	ATCTCCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCTGTAGTTGG	180		
QY	181	TATCAGCAGAGCCAGGCGCAACCTCCCAAGCTCCTGATTTATAGGTTTCTAACCGGGAC	240		
DB	181	TATCAGCAGAGCCAGGCGCAACCTCCCAAGCTCCTGATTTATAGGTTTCTAACCGGGAC	240		
QY	241	TCTGGGGTCCAGACAGATTTCAGGGCAGTGGGGCAGGACAGATTTCACACTGAAATTC	300		
DB	241	TCTGGGGTCCAGACAGATTTCAGGGCAGTGGGGCAGGACAGATTTCACACTGAAATTC	300		
QY	301	AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAAGGACTCCT	360		
DB	301	AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAAGGACTCCT	360		
QY	361	CCCACTTTCCGGGAGGAGGACCAAGTGGAAATCAACAGTACGTTGGCTGCACCATCTGTC	420		
DB	361	CCCACTTTCCGGGAGGAGGACCAAGTGGAAATCAACAGTACGTTGGCTGCACCATCTGTC	420		
QY	421	TTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGTTGTGCTCGCTG	480		
DB	421	TTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGTTGTGCTCGCTG	480		
QY	481	CTGAATACTTCTATCCAGAGAGGCCAAGTACAGTGGAGTGGATACGCCCTCCAA	540		
DB	481	CTGAATACTTCTATCCAGAGAGGCCAAGTACAGTGGAGTGGATACGCCCTCCAA	540		
QY	541	TCGGTTAACTCCAGAGAGTGTCCACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC	600		
DB	541	TCGGTTAACTCCAGAGAGTGTCCACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC	600		
QY	601	AGCAGCACCCCTGACCTCAGCAAGGACAGCTACGAGAAACACAAAGTCTACGGCTCGAA	660		
DB	601	AGCAGCACCCCTGACCTCAGCAAGGACAGCTACGAGAAACACAAAGTCTACGGCTCGAA	660		
QY	661	GTACCCATCAGGGCTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGTGA	720		
DB	661	GTACCCATCAGGGCTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGTGA	720		
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LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Unclassified.					
REFERENCE					
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AUTHORS					
TITLE					
JOURNAL					
Method for producing polyhydroxyalkanoates in recombinant organisms					
Patent: US 6492134-A 5 10-DEC-2002;					
Sequence 5 from patent US 6492134.					
720 bp					
DNA					
linear					
PAT 10-APR-2003					
720 bp					
DNA					
linear					
PAT 27-AUG-2002					
Identification of unique binding interactions between certain					
antibodies and the human B7.1 and B7.2 co-stimulatory antigens.					
BD063036					
BD063036					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
1 (bases 1 to 720)					
AUTHORS					
Anderson, D.R., Hanna, N., Brans, P. and Hard, C.					

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 12:12:30 ; Search time 147.469 Seconds
(without alignments)
13179.730 Million cell updates/sec

Title: US-09-758-173-5
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	100.0	720	19 AAV35486	Macaca primatized
2	720	100.0	720	24 AAS17244	DNA sequence of a
3	718.4	99.8	720	18 AAT62511	Primatized anti-hu
4	622	86.4	720	19 AAV61362	Anti-human Fas hum
5	622	86.4	720	21 AAV78270	Anti-human Fas imm
6	620.4	86.2	891	19 AAV66632	Human immunoglobul
7	620.4	86.2	891	21 AAV78320	Anti-human Fas Ig
8	618.8	85.9	720	19 AAV61360	Anti-human Fas hum

9	618.8	85.9	720	19 AAV61361	Anti-human Fas hum
10	618.8	85.9	720	21 AAA78268	Anti-human Fas imm
11	618.8	85.9	720	21 AAA78269	Anti-human Fas imm
12	617.2	85.7	720	19 AAV61359	Anti-human Fas hum
13	617.2	85.7	720	21 AAA78267	Anti-human Fas imm
14	606	84.2	1081	24 ABS51811	Human mdot cDNA in
15	601.2	83.5	963	22 AAF44895	Human breast cance
16	599.4	83.2	720	21 AAA13924	Human PTHrp monocl
17	599.4	83.2	720	21 AAA13926	Human PTHrp monocl
18	598.8	83.2	720	21 AAA13927	Human PTHrp monocl
19	598.2	83.1	720	21 AAA13928	Human PTHrp monocl
20	596.6	82.9	720	21 AAA13929	Human PTHrp monocl
21	595.4	82.7	720	21 AAA13925	Human PTHrp monocl
22	593.4	82.4	720	21 AAA13922	Human PTHrp monocl
23	591.6	82.2	720	21 AAA13921	Human PTHrp monocl
24	588.4	81.7	968	25 ACC51063	Human Calx protein
25	587.8	81.6	720	21 AAA13928	Human PTHrp monocl
26	587.8	81.6	720	21 AAA13929	Human PTHrp monocl
27	582.2	80.9	772	20 AAZ24418	Human bladder tumo
28	566.4	78.7	648	25 ABZ22307	S. pneumoniae PPS-
29	563.2	78.2	714	25 ABZ24638	Humanised 10D5 ant
30	561.2	77.9	726	17 AAT18060	Monoclonal antibod
31	558	77.5	720	21 ABK10999	DNA encoding prote
32	554.6	77.0	717	18 AAT62934	Murine anti-porcine
33	554.6	77.0	5300	18 AAT62938	3F4 human IgG4 exp
34	553.8	76.9	717	25 ABZ24632	Humanised 3D6 anti
35	551.6	76.6	925	21 AAZ27395	Human IGFAM-15 imm
36	549.2	76.3	740	22 AAF63373	Humanised 323/A3 (
37	549.2	76.3	740	22 AAF63377	Anti-Ep-CAM antibo
38	541	75.1	649	25 ABZ23113	S. pneumoniae PPS-
39	533	74.0	663	22 AAD20744	Human recombinant
40	533	74.0	663	25 ABX79099	Mucin 1 (MUC-1) b1
41	527.6	73.3	737	13 AAO25691	Sequence of the ch
42	520.6	72.3	799	24 AAD32341	Human lung specifi
43	519.2	72.1	727	21 AAZ87965	Chimeric 6G4.2.5 a
44	519.2	72.1	729	16 AAT03380	Anti-IL-8 chimeric
45	519.2	72.1	729	18 AAV03226	Murine variable re

ALIGNMENTS

RESULT 1

AAV35486 standard; DNA; 720 BP.
AAV35486;
29-SEP-1998 (first entry)
Macaca primatized 7B6 light chain DNA.

Monoclonal antibody; Mab; macaque; light chain; antigen; CD80;
CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
T cell proliferation; ss.

Macaca fascicularis.
OS
Key Location/Qualifiers
CDS 1..720
FT /*tag= a
FT /product= 7B6 light chain

WO9819706-A1.
14-MAY-1998.
29-OCT-1997; 97WO-US19906.
08-NOV-1996; 96US-0746361.

PA (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Bams P, Hanna N;
 PI WPI: 1998-286601/25.
 XX P-PSDB; AA063762.
 DR
 DR
 DR
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 XX Example 7: Fig 4a; 87pp; English.
 PS
 PS
 CC This sequence encodes a primatized form of the antibody 7B6 light chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 XX Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;
 SQ

Query Match
 Best local Similarity 100.0%; Score 720; DB 19; Length 720;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCTGCTCAGCTCCCTCGGGCTGCTATGCTGCTCCCGGGTCCAGTGGG 60
 DB 1 ATGAGCTCCCTGCTCAGCTCCCTCGGGCTGCTATGCTGCTCCCGGGTCCAGTGGG 60

QY 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCCTCCCATCAGTGGAGAGCGCGCTCC 120
 DB 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCCTCCCATCAGTGGAGAGCGCGCTCC 120

QY 121 ATCTCTGTAGTCTAGTCTCAAGCTTAAACAGCTTAATGGAGACACCTTCTGAGTTGG 180
 DB 121 ATCTCTGTAGTCTAGTCTCAAGCTTAAACAGCTTAATGGAGACACCTTCTGAGTTGG 180

QY 181 TATCAGAGAGCGGAGCGCAAGCTCCAGGCTCCTGATTTATAGGTTTCTAACCGGGAC 240
 DB 181 TATCAGAGAGCGGAGCGCAAGCTCCAGGCTCCTGATTTATAGGTTTCTAACCGGGAC 240

QY 241 TCTGGGGTCCACAGAGATTACAGCGCTGAGGGGAGGAGGAGATTTCACACTGAAATC 300
 DB 241 TCTGGGGTCCACAGAGATTACAGCGCTGAGGGGAGGAGGAGATTTCACACTGAAATC 300

QY 301 AGCGCAGTGGAGCTGAAGATGTGGGGTTATTTCTCGGGCAAGGTACAGGACTCCT 360
 DB 301 AGCGCAGTGGAGCTGAAGATGTGGGGTTATTTCTCGGGCAAGGTACAGGACTCCT 360

QY 361 CCACATTTCCGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 DB 361 CCACATTTCCGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

QY 421 TTCACTCTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACGTCCTCTGTTGTGGCTG 480
 DB 421 TTCACTCTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACGTCCTCTGTTGTGGCTG 480

QY 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGGTACAGTGGAGGTGATTAAGCGCTCCAA 540
 DB 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGGTACAGTGGAGGTGATTAAGCGCTCCAA 540

481 CTGAATAACTTCTATCCAGAGAGGCGCAAGGTACAGTGGAGGTGATTAAGCGCTCCAA 540
 541 TCGGGTAACTCCAGGAGAGGTGTACAGAGCAGGACAGCAAGGACAGCAGCCTACAGCCTC 600
 541 TCGGGTAACTCCAGGAGAGGTGTACAGAGCAGGACAGCAAGGACAGCAGCCTACAGCCTC 600
 601 ACAGCAGCCTCAGCCTGAGCAGCAAGCAGCAGTACAGCAAGCAAGCAAGTCTAGCCTCGAA 660
 601 ACAGCAGCCTCAGCCTGAGCAGCAAGCAGCAGTACAGCAAGCAAGCAAGTCTAGCCTCGAA 660
 661 GTACCCCATCAGGGCTGAGCTCGCCCGCTCAAGAGCTTCAACAGGGAGAGTGTGA 720
 661 GTACCCCATCAGGGCTGAGCTCGCCCGCTCAAGAGCTTCAACAGGGAGAGTGTGA 720

RESULT 2
 AAS17244
 ID AAS17244 standard; DNA: 720 BP.
 XX AAS17244;
 AC
 XX 12-MAR-2002 (first entry)
 DT
 XX DNA sequence of a primatized form of the light chain of 7B6 antibody.
 DE
 XX Human; macaque monkey; light chain; primatized antibody; 7B6 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; ds.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..720
 FT /tag= a
 FT /product= "Light chain of 7B6 antibody"
 XX
 PN WO200189567-A1.
 XX
 PD 29-NOV-2001.
 XX
 XX 22-MAY-2001; 2001WO-US16364.
 XX
 XX 22-MAY-2000; 2000US-0576424.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX Anderson DR, Hanna N, Bams P;
 PI
 XX WPI: 2002-089895/12.
 DR
 DR P-PSDB; AA011540.
 XX
 XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy.
 XX
 XX Example 8: Fig 4a; 89pp; English.
 PS
 XX The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus,
 CC type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:05:20 ; Search time 1190.71 Seconds
(without alignments)
14696.420 Million cell updates/sec

Title: US-09-758-173-5
Perfect score: 720
Sequence: 1 ATGACCTCCCTGCTCAGCT.....TCACACGGGAGAGTGTTGA 720

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	618.8	85.9	816	12	BI759427 603043095
2	610.6	84.8	774	12	BM007808 603617276
3	608	84.4	795	14	CB958667 603617276
4	598.2	83.1	857	12	BI758820 603042739

5	597.2	82.9	918	10	BG681688 602627806
6	595.4	82.7	734	14	CB957433 AGENCOURT
7	594.4	82.6	898	13	BQ708918 AGENCOURT
8	592.4	82.3	726	12	BM007723 603617168
9	592	82.2	796	14	CB956719 AGENCOURT
10	591.8	82.2	995	13	BQ712430 AGENCOURT
11	590.8	82.1	952	10	BG758592 602712820
12	587.2	81.6	720	12	BI768966 603058111
13	587	81.5	785	12	CB958366 AGENCOURT
14	585.8	81.4	734	14	CB984409 AGENCOURT
15	578.4	80.3	908	10	BG685179 602637065
16	578	80.3	859	10	BG758795 602713155
17	576.6	80.1	771	14	CB956254 AGENCOURT
18	574	79.7	731	14	CB985070 AGENCOURT
19	570.6	79.2	958	13	BQ709417 AGENCOURT
20	570.2	79.2	880	10	BG755003 602711509
21	569.2	79.1	765	14	CB957191 AGENCOURT
22	567.4	78.8	701	10	BG547597 AGENCOURT
23	565.8	78.6	738	10	BG740066 602631139
24	564.6	78.4	730	12	BI837183 AGENCOURT
25	563.2	78.2	734	14	CB986286 AGENCOURT
26	559.2	77.7	766	14	CB956983 AGENCOURT
27	558.6	77.6	753	10	BG756401 602715727
28	557.2	77.4	880	10	BG757588 AGENCOURT
29	555.6	77.2	875	12	BI518518 AGENCOURT
30	554.8	77.1	907	13	BQ708655 AGENCOURT
31	553.6	76.9	710	12	BI908471 AGENCOURT
32	551.6	76.6	743	14	CB957685 AGENCOURT
33	549.6	76.3	931	10	BG757255 AGENCOURT
34	549.2	76.3	811	14	CB956301 AGENCOURT
35	547.4	76.0	687	14	CB552296 MMSP0044
36	547.4	76.0	696	12	BI838136 603083638
37	544.2	75.6	970	13	BI837518 603083638
38	542.4	75.3	716	12	BI908319 603066141
39	542	75.3	912	10	BF974515 602243421
40	540.8	75.1	693	14	CB956992 AGENCOURT
41	540.4	75.1	760	14	CB986353 AGENCOURT
42	540.2	75.0	817	14	CB957285 AGENCOURT
43	538.8	74.8	653	9	AM404795 UI-HF-BLO
44	538.4	74.8	1009	13	BU146853 AGENCOURT
45	538.2	74.8	925	13	BI837517 603083638

ALIGNMENTS

RESULT 1
BI759427
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI759427 816 bp mRNA linear EST 25-SEP-2001
603043095F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183446 5',
mRNA sequence.
BI759427
BI759427.1 GI:15751005
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 816)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11457 row: n column: 23
High quality sequence start: 2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: October 2, 2003, 13:10:05 ; Search time 38.2657 Seconds
(without alignments)
8304.972 Million cell updates/sec

Title: US-09-758-173-5
Perfect score: 720
Sequence: 1 ATGAGCTCCCTGCTCAGCT.....TCAATAGGGGAGAGTGTTCGA 720

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*

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5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	720	100.0	720	3	US-08-487-550-5
2	720	100.0	720	4	US-09-526-098-5
3	519.2	72.1	729	1	US-08-398-613A-55
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5	519.2	72.1	729	1	US-08-398-611A-55
6	519.2	72.1	729	1	US-08-396-851A-55
7	519.2	72.1	729	2	US-08-491-334A-55
8	519.2	72.1	729	3	US-09-027-449-41
9	519.2	72.1	729	3	US-08-804-444A-41
10	519.2	72.1	729	3	US-09-026-985-41
11	519.2	72.1	729	4	US-09-121-952A-41
12	519.2	72.1	729	4	US-09-234-340A-41
13	489.4	68.0	5703	1	US-08-467-420A-50
14	489.4	68.0	5703	1	US-08-470-110A-50
15	489.4	68.0	5703	1	US-08-667-769A-50
16	489.4	68.0	5703	2	US-08-940-371-50
17	489.4	68.0	5703	2	US-08-637-647-50
18	489.4	68.0	5703	5	PCT-US95-17082A-50
19	486.4	67.6	19040	4	US-09-343-485A-3
20	474.8	65.9	931	3	US-09-049-672A-19
21	471.6	65.5	1066	1	US-08-157-101A-4
22	468.8	65.1	705	1	US-08-488-376-16
23	468.8	65.1	705	2	US-08-634-223-16
24	468.8	65.1	705	2	US-08-634-400-16
25	468.8	65.1	705	2	US-08-635-878-16
26	468.8	65.1	705	2	US-08-770-057-16
27	468.8	65.1	705	2	US-08-770-057-16

28	468.8	65.1	705	3	US-09-335-697B-16
29	468.8	65.1	705	4	US-09-335-697B-16
30	468.8	65.1	705	4	US-09-740-002-16
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36	462	64.2	729	1	US-08-899-575-152
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38	462	64.2	729	5	PCT-US95-08743-156
39	462	64.2	13254	1	US-08-276-852-170
40	462	64.2	13254	1	US-08-276-852-170
41	462	64.2	13254	1	US-08-899-575-156
42	462	64.2	13254	1	US-08-899-575-170
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45	462	64.2	13254	5	PCT-US95-08743-156

ALIGNMENTS

RESULT 1
US-08-487-550-5
; Sequence 5, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/487,550
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..720
; US-08-487-550-5

Query Match

100.0% Score 720; DB 3; Length 720;

Best Local Similarity 100.0%; Pred. No. 4e-203;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTGCTATTGCTGCTGCTCCCGGGTCCAGTGG 60
Db 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTGCTATTGCTGCTGCTCCCGGGTCCAGTGG 60

QY 61 GAAGTTGTGAGTCACTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 120
Db 61 GAAGTTGTGAGTCACTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 120

QY 121 ATCTCCTCTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGACACCTTCTCTGAGTTGG 180
Db 121 ATCTCCTCTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGACACCTTCTCTGAGTTGG 180

QY 181 TATCAGCAGACGAGGCAACCTCCAAAGCTCTGATTTTATAGTTTCTTACCGGGAC 240
Db 181 TATCAGCAGACGAGGCAACCTCCAAAGCTCTGATTTTATAGTTTCTTACCGGGAC 240

QY 241 TCTGGGGTCCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTCACACTGAAATC 300
Db 241 TCTGGGGTCCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTCACACTGAAATC 300

QY 301 AGCGAGTGGAGGCTGAGATGTTGGGTTTATTTCTCGGGCAAGTACAGGACTCCT 360
Db 301 AGCGAGTGGAGGCTGAGATGTTGGGTTTATTTCTCGGGCAAGTACAGGACTCCT 360

QY 361 CCCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 420
Db 361 CCCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 420

QY 421 TTCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 480
Db 421 TTCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 480

QY 481 CTGAATAACTTCTATCCAGAGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
Db 481 CTGAATAACTTCTATCCAGAGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540

RESULT 2
US-09-526-098-5
Sequence 5, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-8620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..720
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..720
US-09-526-098-5

Query Match 100.0%; Score 720; DB 4; Length 720;
Best Local Similarity 100.0%; Pred. No. 4e-203;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTGCTATTGCTGCTGCTCCCGGGTCCAGTGG 60
Db 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTGCTATTGCTGCTGCTCCCGGGTCCAGTGG 60

QY 61 GAAGTTGTGAGTCACTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 120
Db 61 GAAGTTGTGAGTCACTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 120

QY 121 ATCTCCTCTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGACACCTTCTCTGAGTTGG 180
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QY 181 TATCAGCAGACGAGGCAACCTCCAAAGCTCTGATTTTATAGTTTCTTACCGGGAC 240
Db 181 TATCAGCAGACGAGGCAACCTCCAAAGCTCTGATTTTATAGTTTCTTACCGGGAC 240

QY 241 TCTGGGGTCCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTCACACTGAAATC 300
Db 241 TCTGGGGTCCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTCACACTGAAATC 300

QY 301 AGCGAGTGGAGGCTGAGATGTTGGGTTTATTTCTCGGGCAAGTACAGGACTCCT 360
Db 301 AGCGAGTGGAGGCTGAGATGTTGGGTTTATTTCTCGGGCAAGTACAGGACTCCT 360

QY 361 CCCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 420
Db 361 CCCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 420

QY 421 TTCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 480
Db 421 TTCACTTTCCGCGAGGACCAAGTGGGAAATCAAAAGCTACGCTGCTGCTGCTGCTGCTG 480

QY 481 CTGAATAACTTCTATCCAGAGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
Db 481 CTGAATAACTTCTATCCAGAGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: October 2, 2003, 19:53:01 ; Search time 142.434 Seconds
(without alignments)
12894.584 Million cell updates/sec

Title: US-09-758-173-5
Perfect score: 720
Sequence: 1 ATGAGCTCCTCTCAGCT.....TCACAGGAGAGTTCGA 720

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PTCUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	720	100.0	720	10	US-09-948-429B-5
2	720	100.0	720	12	US-10-124-907-5
3	720	100.0	720	12	US-10-291-532-5
4	720	100.0	720	13	US-10-124-905-5
5	720	100.0	720	13	US-10-073-138-3
6	607.4	84.4	2272	14	US-10-158-646-63
7	588.4	81.7	968	11	US-09-992-600A-7
8	588.4	81.7	968	11	US-09-924-340-7
9	588.4	81.7	968	12	US-09-992-095B-7
10	588.4	81.7	968	12	US-10-154-678-7
11	588.4	81.7	968	12	US-09-999-570-7
12	588.4	81.7	968	14	US-10-000-489-7
13	588.4	81.7	968	14	US-10-000-986-7
14	585.2	81.3	738	14	US-10-158-646-61
15	557.8	77.5	657	11	US-09-972-656-91
16	546.6	75.9	657	11	US-09-972-656-103

17	535.4	74.4	657	11	US-09-972-656-105
18	533.8	74.1	657	11	US-09-972-656-93
19	533	74.0	663	10	US-08-822-898A-25
20	520.6	72.3	799	11	US-09-909-567B-14
21	519.2	72.1	729	11	US-09-726-258-41
22	504	70.0	1775	14	US-10-158-646-64
23	500	69.4	717	14	US-10-171-452A-37
24	500	69.4	717	14	US-10-171-452A-55
25	498.4	69.2	717	14	US-10-171-452A-43
26	498.4	69.2	717	14	US-10-171-452A-49
27	497	69.0	1033	9	US-09-799-514-2
28	494	68.6	928	14	US-10-221-945-5
29	488.8	67.9	708	14	US-10-153-382-6
30	487.4	67.7	788	14	US-10-158-646-58
31	486	67.5	705	14	US-10-153-382-14
32	484	67.2	768	12	US-10-384-933-106
33	484	67.2	768	12	US-10-384-933-108
34	484	67.2	768	14	US-10-216-484-106
35	484	67.2	768	14	US-10-216-484-108
36	483.6	67.2	702	14	US-10-150-475A-5
37	482.4	67.0	768	12	US-10-384-933-51
38	482.4	67.0	768	12	US-10-384-933-53
39	482.4	67.0	768	14	US-10-216-484-51
40	482.4	67.0	768	14	US-10-216-484-53
41	480.8	66.8	768	12	US-10-384-933-49
42	480.8	66.8	768	14	US-10-216-484-49
43	480	66.7	702	14	US-10-153-382-10
44	479.4	66.6	1775	14	US-10-158-646-64
45	479.2	66.6	913	10	US-09-822-830A-531

ALIGNMENTS

RESULT 1

US-09-948-429B-5
Sequence 5, Application US/09948429B
Patent No. US2002017689A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948.429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

Sequence 105, Appl
Sequence 93, Appl
Sequence 25, Appl
Sequence 11, Appl
Sequence 41, Appl
Sequence 64, Appl
Sequence 37, Appl
Sequence 43, Appl
Sequence 55, Appl
Sequence 49, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 58, Appl
Sequence 14, Appl
Sequence 106, App
Sequence 108, App
Sequence 108, App
Sequence 5, Appl
Sequence 51, Appl
Sequence 53, Appl
Sequence 51, Appl
Sequence 53, Appl
Sequence 49, Appl
Sequence 48, Appl
Sequence 10, Appl
Sequence 64, Appl
Sequence 531, App

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; NAME/KEY: mat_peptide
; LOCATION: 1..720
; US-09-948-429B-5

Query Match 100.0%; Score 720; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 2.2e-221;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCCTGCGGCTGCTATTCCTGCTCCCTGCGGCTCCAGTGGG 60
DB 1 ATGAGCCTCCCTGCTCAGCTCCCTGCGGCTGCTATTCCTGCTCCCTGCGGCTCCAGTGGG 60

QY 61 GAAGTTGTGATGACTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCC 120
DB 61 GAAGTTGTGATGACTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCC 120

QY 121 ATCTCTGTAGTCTAGTCAAGCCCTTAACACACAGTAAATGAGACACTTCTCTGAGTTGG 180
DB 121 ATCTCTGTAGTCTAGTCAAGCCCTTAACACACAGTAAATGAGACACTTCTCTGAGTTGG 180

QY 181 TATCAGCAGAGCCAGGCGCACTCCAGGCTCCCTGATTTATAAGTTTCTTAACCGGAC 240
DB 181 TATCAGCAGAGCCAGGCGCACTCCAGGCTCCCTGATTTATAAGTTTCTTAACCGGAC 240

QY 241 TCTGGGTCCCGACAGAGATTTCAGGGCAGTGGGCGCAGGACAGATTTTCACACTGAAATC 300
DB 241 TCTGGGTCCCGACAGAGATTTCAGGGCAGTGGGCGCAGGACAGATTTTCACACTGAAATC 300

QY 301 AGGCGAGTGGAGCTGAAGATGTTGGGTTTATTTCTCGGGCAAGGTACAGGACTCCT 360
DB 301 AGGCGAGTGGAGCTGAAGATGTTGGGTTTATTTCTCGGGCAAGGTACAGGACTCCT 360

QY 361 CCACATTTCTGCGGAGGAGCCAAAGTGGAAATCAACCTACGTTGGTGGTGCACCTCTGTC 420
DB 361 CCACATTTCTGCGGAGGAGCCAAAGTGGAAATCAACCTACGTTGGTGGTGCACCTCTGTC 420

QY 421 TTCTATCTCCCGCATCTCTGATGAGCAGTTGAAATCTGGAATCTGCTGTTGTTGCTG 480
DB 421 TTCTATCTCCCGCATCTCTGATGAGCAGTTGAAATCTGGAATCTGCTGTTGTTGCTG 480

QY 481 CTGAATTAATCTTATCTCCAGAGAGGCGCAAGTACAGTGAAGTGGATAGCCCTCCAA 540
DB 481 CTGAATTAATCTTATCTCCAGAGAGGCGCAAGTACAGTGAAGTGGATAGCCCTCCAA 540

QY 541 TCGGGTAACTTCCAGAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600
DB 541 TCGGGTAACTTCCAGAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600

QY 601 AGCAGCAGCCTGACCTGAGCAAGAGCAGTACGAGTACGAGTACGAGTACGAGTACGAG 660
DB 601 AGCAGCAGCCTGACCTGAGCAAGAGCAGTACGAGTACGAGTACGAGTACGAGTACGAG 660

QY 661 GTCAACCATCAGGCGCTGAGCTGCGGCGCTCAACAGAGAGCTTCAACAGGAGAGTGTGA 720
DB 661 GTCAACCATCAGGCGCTGAGCTGCGGCGCTCAACAGAGAGCTTCAACAGGAGAGTGTGA 720

RESULT 2

US-10-124-807-5
; Sequence 5, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; NAME/KEY: mat_peptide
; LOCATION: 1..720
; US-10-124-807-5

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Best Local Similarity 100.0%; Pred. No. 2.2e-221;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCCTGCGGCTGCTATTCCTGCTCCCTGCGGCTCCAGTGGG 60
DB 1 ATGAGCCTCCCTGCTCAGCTCCCTGCGGCTGCTATTCCTGCTCCCTGCGGCTCCAGTGGG 60

QY 61 GAAGTTGTGATGACTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCC 120
DB 61 GAAGTTGTGATGACTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCC 120

QY 121 ATCTCTGTAGTCTAGTCAAGCCCTTAACACACAGTAAATGAGTATTAAGTTTCTTAACCGGAC 240
DB 121 ATCTCTGTAGTCTAGTCAAGCCCTTAACACACAGTAAATGAGTATTAAGTTTCTTAACCGGAC 240

QY 181 TATCAGCAGAGCCAGGCGCACTCCAGGCTCCCTGATTTATAAGTTTCTTAACCGGAC 240
DB 181 TATCAGCAGAGCCAGGCGCACTCCAGGCTCCCTGATTTATAAGTTTCTTAACCGGAC 240

QY 241 TCTGGGTCCCGACAGAGATTTCAGGGCAGTGGGCGCAGGACAGATTTTCACACTGAAATC 300
DB 241 TCTGGGTCCCGACAGAGATTTCAGGGCAGTGGGCGCAGGACAGATTTTCACACTGAAATC 300

Result No.	Query %	Score	Match	Length	DB	ID	Description
1	1242	100.0	239	18	AAW01819		Prima ^{tised} anti-hu
2	1242	100.0	239	19	AAW63762		Macaque prima ^{tized}
3	1242	100.0	239	23	AAU11540		Protein sequence o
4	1116	89.9	239	19	AAW71879		Anti-human Fas hum
5	1116	89.9	239	21	AAAB12916		Anti-human Fas hum
6	1113	89.6	239	19	AAW71877		Anti-human Fas hum
7	1113	89.6	239	19	AAW71878		Anti-human Fas hum
8	1113	89.6	239	21	AAAB12914		Anti-human Fas imm
9	1113	89.6	239	21	AAAB12915		Anti-human Fas imm

DR WPI: 1997-108638/10.
 DR N-PSDB; AAT62511.
 XX
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen
 PT useful for treating autoimmune disease or graft-versus-host disease
 XX
 PS Claim 8; Fig 9A; 81pp; English.
 XX
 CC 2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy
 CC variable genes (see also AAT62511 and AAT13847) are inserted into
 CC an expression vector (pref. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
 CC antibodies have also been produced (see also AAW01817-19 and
 CC AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway,
 CC making them useful immunosuppressants for the treatment of
 CC autoimmune disorders and graft-versus-host disease.
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 SQ Sequence 239 AA;
 Query Match 100.0%; Score 1242; DB 18; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.8e-69;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLPAQLGLLLCVPGSGEVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60
 DB 1 MSLPAQLGLLLCVPGSGEVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60
 QY 61 YQKPGQPPRLIIKYVNSRDGVPDRFSGSGAGTDTLKISAVEADGVYFCGGGTTP 120
 DB 61 YQKPGQPPRLIIKYVNSRDGVPDRFSGSGAGTDTLKISAVEADGVYFCGGGTTP 120
 QY 121 PTFGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPRKAYQWKVDNALQ 180
 DB 121 PTFGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPRKAYQWKVDNALQ 180
 QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGEC 239
 DB 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGEC 239
 RESULT 2
 AAW63762
 ID AAW63762 standard; Protein; 239 AA.
 AC AAW63762;
 XX
 XX 29-SEP-1998 (first entry)
 DE
 XX Macaque primatised 7B6 light chain protein.
 XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation.
 XX
 XX Macaca fascicularis.
 OS
 XX W09819706-A1.
 XX
 XX 14-MAY-1998.
 PD
 XX 29-OCT-1997; 97WO-US19906.
 XX
 XX 08-NOV-1996; 96US-0746361.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX Anderson DR, Brams P, Hanna N;
 XX
 XX

DR WPI: 1998-286601/25.
 DR N-PSDB; AAV35486.
 XX
 PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 PS Example 7; Fig 4a; 87pp; English.
 XX
 CC This sequence represents a primatised form of the antibody 7B6 light
 CC chain from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC MAB's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC MAB can be conjugated to a drug or toxin. MAB's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. MAB's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 1242; DB 19; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.8e-69;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLPAQLGLLLCVPGSGEVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60
 DB 1 MSLPAQLGLLLCVPGSGEVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60
 QY 61 YQKPGQPPRLIIKYVNSRDGVPDRFSGSGAGTDTLKISAVEADGVYFCGGGTTP 120
 DB 61 YQKPGQPPRLIIKYVNSRDGVPDRFSGSGAGTDTLKISAVEADGVYFCGGGTTP 120
 QY 121 PTFGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPRKAYQWKVDNALQ 180
 DB 121 PTFGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPRKAYQWKVDNALQ 180
 QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGEC 239
 DB 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSNRGEC 239
 RESULT 3
 AAU11540
 ID AAU11540 standard; Protein; 239 AA.
 XX
 AC AAU11540;
 XX
 XX 12-MAR-2002 (first entry)
 DE
 XX Protein sequence of primatised form of the light chain of 7B6 antibody.
 XX Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.
 XX
 XX Chimeric - Homo sapiens.
 OS
 XX Chimeric - Macaca sp.
 OS
 XX Synthetic.
 XX

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 09:07:34 ; Search time 10.503 seconds
(without alignments)
2188.349 Million cell updates/sec

Title: us-09-758-173-6
Perfect score: 1242
Sequence: 1 MSLPAQLGLLLCVPGSSG.....EVTHQGLSPVTKSFNRGEC 239
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*\n1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	915	73.7	215	2 JE0244	Ig kappa chain NIG
2	908	73.1	215	2 JE0242	Ig kappa chain NIG
3	876	70.5	215	2 JE0243	Ig kappa chain NIG
4	860	69.2	215	2 A23746	Ig kappa chain V-I
5	841.5	67.8	216	2 JE0241	Ig kappa chain Am3
6	820	66.0	219	2 S52028	Ig kappa chain - m
7	807	65.0	219	2 PC4203	Ig kappa chain (mo
8	806	64.9	219	2 S16112	Ig kappa chain V r
9	796	64.1	219	2 S38865	Ig kappa chain - m
10	795	64.0	217	2 S42772	Ig kappa chain - m
11	770	62.0	225	2 JL0029	Ig kappa chain pre
12	765.5	61.6	240	2 S06084	Ig kappa chain pre
13	723.5	58.3	220	2 A31790	Ig kappa chain V r
14	702	56.5	225	2 S37484	Ig kappa chain - m
15	694.5	55.9	218	2 S68241	Ig kappa chain V r
16	688.5	55.4	214	2 JC5810	Ig kappa chain (Ma
17	688.5	55.4	218	2 S68212	Ig kappa chain (Ma
18	687.5	55.4	234	2 S14237	monoclonal antibody
19	686	55.2	197	2 S28593	Ig kappa chain pre
20	684.5	55.1	234	2 S01320	Ig kappa chain (WM
21	680	54.8	230	2 S33161	Ig kappa chain pre
22	662.5	53.3	210	2 A56169	Ig kappa chain - s
23	644	51.9	235	2 S25058	Ig kappa chain V r
24	617	49.7	178	2 PT0219	Ig kappa chain - m
25	599	48.2	135	2 S52059	Ig kappa chain V-C
26	572	46.1	229	2 A20969	JC-kappa protein
27	565.5	45.5	140	2 S22658	Ig kappa chain pre
28	552	44.4	133	2 S23230	Ig kappa chain pre
29	552	44.4	133	2 S42611	HUNVK protein prec

30	552	44.4	136	2 S40357	Ig kappa chain V-J
31	550	44.3	133	1 K2HURP	Ig kappa chain pre
32	549	44.2	133	2 S40324	Ig kappa chain V r
33	548	44.1	106	1 K3RU	Ig kappa chain C r
34	548	44.1	142	2 S22902	Ig kappa chain V r
35	541	43.6	135	2 S40342	Ig kappa chain - h
36	538	43.3	133	1 A24452	Ig kappa chain pre
37	537	43.2	132	2 S26882	Ig kappa chain V r
38	534	42.9	128	2 S40373	Ig kappa chain - h
39	533	42.9	238	2 A49633	Ig kappa chain - h
40	524	42.2	126	2 S40312	Ig lambda-like cha
41	520	41.9	132	2 S40322	Ig kappa chain - h
42	519.5	41.8	131	2 S40355	Ig kappa chain - h
43	513	41.3	99	2 A37927	Ig kappa chain C r
44	510.5	41.1	144	2 PL0106	Ig kappa chain pre
45	508.5	40.9	132	2 PH0106	anti-digoxin trans

ALIGNMENTS

RESULT 1
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 915; DB 2; Length 215;
Best Local Similarity 80.9%; Pred. No. 2e-55; 17; Indels 6; Gaps 3;
Matches 178; Conservative 19; Mismatches 19;

QY	21	EVVMTQSLPLITPEGPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD	80
DB	1	EVVLTQSPATLSVSPGERATLSCRAQSV-HSN---LAWYQKPGQAPRLIIYRASTRA	55
QY	81	SGVPDRFSSGGAGTFTLKISAREADYGVFCGGGTTPP-TRGGGTGVKVIKRTVAAPS	139
DB	56	TGIPARFSGSGSGTDFTLTSSLSQSEDFALYICQYQNTWPLTFGGGTGVKVIKRTVAAPS	115
QY	140	VFIFPPSDQLKSGTASVYVCLLNNFYPREAKYQWKVDNALQSGNSQESVTEQDSKDS	199
DB	116	VFIFPPSDQLKSGTASVYVCLLNNFYPREAKYQWKVDNALQSGNSQESVTEQDSKDS	175
QY	200	LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC	239
DB	176	LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC	215

RESULT 2
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 908; DB 2; Length 215;
 Best Local Similarity 79.9%; Pred. No. 5,9e-55;
 Matches 175; Conservative 19; Mismatches 21; Indels 4; Gaps 1;

QY 21 EYVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVNDRD 80
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVN---YLAAYQKPGQAPRLIIYDASSRA 56
 QY 81 SGVPDRFSGSGAGTFTLKISAVEAEDGVVFCGGTPTPTFGGKVEIKRTVAAPSV 140
 DB 57 TGIPIRFGSGSGTDFLTISGLEPDAVYVCOQYDRPPWTFGGTKVEIKRTVAAPSV 116
 QY 141 FIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 DB 117 FIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 176
 QY 201 SSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 239
 DB 177 SSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 215

RESULT 3
 JE0243
 Ig kappa chain NIG93 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0243
 R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazil, H.; T
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
 A:Reference number: JE0243
 A:Accession: JE0243
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 876; DB 2; Length 215;
 Best Local Similarity 77.7%; Pred. No. 8,9e-53;
 Matches 171; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

QY 21 EYVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVNDRD 80
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSV-----TNYVYMQRLGAPRLIIYDASTRA 55
 QY 81 SGVPDRFSGSGAGTFTLKISAVEAEDGVVFCGGTPTPTFGGKVEIK-RTVAAPS 139
 DB 56 TGVPIRFGSGSGTFTLTISLSQSDPAIYVCOQHNNWPTFGGKVEIKRTVAAPS 115
 QY 140 VFIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 199
 DB 116 VFIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 175
 QY 200 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 239
 DB 176 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 215

RESULT 4
 A23746
 Ig kappa chain V-III (KAU cold agglutinin) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
 C:Accession: A23746
 R:Leoni, J.; Ghiso, J.; Gori, F.; Frangione, B.
 J. Biol. Chem. 266, 2836-2842, 1991
 A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
 A:Reference number: A23746; MUID:91131575; PMID:1993660
 A:Accession: A23746
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-215 <LEO>

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 860; DB 2; Length 215;
 Best Local Similarity 78.4%; Pred. No. 1.1e-51;
 Matches 171; Conservative 18; Mismatches 25; Indels 4; Gaps 1;

QY 21 EYVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVNDRD 80
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSV---SSNLAWYQKPGQAPRLIIYDASSRA 56
 QY 81 SGVPDRFSGSGAGTFTLKISAVEAEDGVVFCGGTPTPTFGGKVEIKRTVAAPSV 140
 DB 57 TGIPIRFGSGSGTDFLTISGLEPDAVYVCOQYDRPPWTFGGTKVEIKRTVAAPSV 116
 QY 141 FIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 DB 117 FIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 176
 QY 201 SSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
 DB 177 SSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 214

RESULT 5
 JE0241
 Ig kappa chain Am37 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0241

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
 submitted to JIPID, November 1998
 A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
 A:Reference number: JE0241
 A:Accession: JE0241
 A:Molecule type: protein
 A:Residues: 1-216 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 841.5; DB 2; Length 216;
 Best Local Similarity 76.7%; Pred. No. 2e-50;
 Matches 168; Conservative 21; Mismatches 27; Indels 3; Gaps 3;

QY 21 EYVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVNDRD 80
 DB 1 DIVLTQSPDLAVSLGERATINCKSSQSVLY-NSKNFLAWYQKPGQ-PKLLIW-ANVRE 57
 QY 81 SGVPDRFSGSGAGTFTLKISAVEAEDGVVFCGGTPTPTFGGKVEIKRTVAAPSV 140
 DB 58 SGVPDRFSGSGTDFLTISNLQELVAVYVCOQYVSTPISFGGGRLEIKRTVAAPSV 117
 QY 141 FIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 DB 118 FIFPPSDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKDYSL 177
 QY 201 SSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 239
 DB 178 SSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 216

RESULT 6
 S52028
 Ig kappa chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S52028

R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosen, J.; Dirkse, W.G.; Schots, A
 submitted to the EMBL Data Library, August 1994
 A:Description: Coordinate expression of antibody subunit genes yields high levels of
 A:Reference number: S52028
 A:Accession: S52028

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 6.59233 Seconds
(without alignments)
1704.917 Million cell updates/sec

Title: US-09-758-173-6
Perfect score: 1242
Sequence: 1 MSLPAQLGLLLCPVSSG.....EVTHQGLSSPVTKSFNRGEC 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	550	44.3	133	1	KV2F_HUMAN
2	548	44.1	106	1	KAC_RAT
3	487	39.2	117	1	KV2E_HUMAN
4	471	37.9	113	1	KV2D_MOUSE
5	453	36.5	113	1	KV2B_HUMAN
6	433.5	34.9	112	1	KV2C_HUMAN
7	430	34.6	113	1	KV2L_HUMAN
8	422	34.0	129	1	KV3L_HUMAN
9	420.5	33.9	115	1	KV4B_HUMAN
10	420	33.8	133	1	KV3H_HUMAN
11	414	33.3	129	1	KV3M_HUMAN
12	414	33.3	129	1	KV3W_HUMAN
13	411.5	33.1	134	1	KV4C_MOUSE
14	404	32.5	113	1	KV2E_MOUSE
15	403.5	32.5	131	1	KV3I_MOUSE
16	401	32.3	113	1	KV2F_MOUSE
17	392.5	32.2	132	1	KV3F_MOUSE
18	396.5	31.9	128	1	KV3K_HUMAN
19	389	31.3	112	1	KV2D_MOUSE
20	384.5	31.0	114	1	KV4A_HUMAN
21	372.5	30.0	115	1	KV3I_HUMAN
22	372	30.0	109	1	KV3D_HUMAN
23	369.5	29.8	121	1	KV4D_HUMAN
24	368.5	29.7	111	1	KV3H_MOUSE
25	368.5	29.7	136	1	KV5B_MOUSE
26	368	29.6	113	1	KV2C_MOUSE
27	367	29.5	106	1	KAC_RAT
28	364.5	29.3	111	1	KV3M_MOUSE
29	364.5	29.3	111	1	KV3O_MOUSE
30	364	29.3	109	1	KV3B_HUMAN
31	364	29.3	120	1	KV2B_MOUSE
32	363.5	29.3	111	1	KV3N_MOUSE
33	361	29.1	109	1	KV3F_HUMAN

34	359.5	28.9	108	1	KV1_CANFA
35	359	28.9	106	1	KAC_RAT
36	358.5	28.9	111	1	KV3J_MOUSE
37	358	28.8	110	1	KV3P_MOUSE
38	357.5	28.8	111	1	KV3C_MOUSE
39	357.5	28.8	111	1	KV3Q_MOUSE
40	356.5	28.7	111	1	KV3T_MOUSE
41	354.5	28.5	111	1	KV3L_MOUSE
42	354.5	28.5	111	1	KV3R_MOUSE
43	354.5	28.5	129	1	KV1W_HUMAN
44	354	28.5	109	1	KV3E_HUMAN
45	353	28.4	112	1	KV2A_MOUSE

ALIGNMENTS

RESULT 1
KV2F_HUMAN
ID KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combracio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
CC EMBL; 200020; CAA77315.1; -
CC PIR; A01890; K2HURP.
CC HSP; P80362; IWL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding activity; NAS.
CC GO; GO:0005955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Fram; PF00047; Ig; 1.
CC SMART; SM00406; Igv; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 20
CC CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
CC DOMAIN 21 43 FRAMEWORK-1.
CC DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 60 74 FRAMEWORK-2.
CC DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 82 113 FRAMEWORK-3.
CC DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 123 132 FRAMEWORK-4.
CC DISULFID 43 113 BY SIMILARITY.
CC NON_TER 133 133
CC SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;
SQ
Query Match 44.3%; Score 550; DB 1; Length 133;
Best Local Similarity 80.5%; Pred. No. 1.8e-37;

P01618	canis famil
P01836	rattus norv
P01662	mus musculu
P01668	mus musculu
P01656	mus musculu
P01672	mus musculu
P01664	mus musculu
P01670	mus musculu
P04431	homo sapien
P01623	homo sapien
P01626	mus musculu

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OM protein - protein search, using sw model

Run on: October 2, 2003, 08:56:23 ; Search time 23.129 Seconds
(without alignments)
2666.544 Million cell updates/sec

Title: US-09-758-173-6
Perfect score: 1242
Sequence: 1 MSFPAQLGLLLCVPGSSG.....EVTHQGLSPVTKSPNRGEC 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1103	88.8	239	4	Q8TCD0
2	1086	87.4	239	4	Q8NEK0
3	949.5	76.4	234	4	Q8NEK1
4	864.5	69.6	238	11	Q8VC16
5	843.5	67.9	238	11	Q8VC37
6	808	65.1	239	11	Q8VC55
7	792	63.8	239	11	Q8VC55
8	691.5	55.7	234	11	Q8VCP0
9	682.5	55.0	234	11	Q8VCP0
10	669.5	53.9	234	11	Q8VCP0
11	667	53.7	235	11	Q8VCP0
12	656.5	52.9	234	11	Q8VCP0
13	655.5	52.8	233	11	Q8VCP0
14	638.5	51.4	234	11	Q8VCP0
15	462.5	37.2	114	4	Q9UL80
16	460.5	37.1	233	4	Q8TBC9

17	447	36.0	234	4	Q8N355	Q8n355 homo sapien
18	445	35.8	236	4	Q8NEJ1	Q8nejl homo sapien
19	437.5	35.2	237	4	Q8WU6	Q8wtu6 homo sapien
20	434.5	35.0	237	4	Q8WU4	Q8wuk4 homo sapien
21	427	34.4	104	11	Q9JL82	Q9jl82 mus musculu
22	414.5	33.4	233	4	Q8N5F4	Q8n5f4 homo sapien
23	408	32.9	236	4	Q8E61	Q8e61 homo sapien
24	407.5	32.8	148	11	Q8K122	Q8k122 mus musculu
25	380	30.6	235	11	Q9NM11	Q9nm11 mus musculu
26	379.5	30.6	233	4	Q8E169	Q8e169 homo sapien
27	375	30.2	109	4	Q8UL78	Q8ul78 homo sapien
28	362.5	29.2	240	4	Q8WU3	Q8wuk3 homo sapien
29	353.5	28.5	111	11	Q92039	Q920a9 mus musculu
30	350	28.2	109	4	Q8UL85	Q8ul85 homo sapien
31	342.5	27.6	108	4	Q8UL83	Q8ul83 homo sapien
32	342	27.5	109	4	Q8UL86	Q8ul86 homo sapien
33	333.5	26.9	107	11	Q9ER29	Q9er29 mus musculu
34	329.5	26.5	103	11	Q9JL80	Q9jl80 mus musculu
35	329.5	26.5	108	4	Q8UL79	Q8ul79 homo sapien
36	326	26.2	134	11	Q8VDP0	Q8vd30 mus musculu
37	324	26.1	107	4	Q8E8A9	Q8esa9 homo sapien
38	324	26.1	114	11	Q8K1F1	Q8k1f1 mus musculu
39	322.5	26.0	108	4	Q8UL77	Q8ul77 homo sapien
40	321	25.8	112	11	Q8K1F3	Q8k1f3 mus musculu
41	314.5	25.3	108	4	Q8UL70	Q8ul70 homo sapien
42	314	25.3	112	11	Q8K1F2	Q8k1f2 mus musculu
43	312.5	25.2	99	11	Q8JL74	Q8jl74 mus musculu
44	309.5	24.9	298	11	Q8QVF0	Q8qvf0 mus musculu
45	309	24.9	107	4	Q9UL81	Q9ul81 homo sapien

ALIGNMENTS

RESULT 1

ID	Q8TCD0	PRELIMINARY	PRT	239 AA.
AC	Q8TCD0			
DT	01-JUN-2002 (TREMELrel. 21, Created)			
DT	01-JUN-2002 (TREMELrel. 21, Last sequence update)			
DT	01-MAR-2003 (TREMELrel. 23, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung			
RA	Strasbourg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC022362; AAH22362.1; -			
DR	InterPro; IPR007110; Ig-Like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_2.			
DR	SMART; SM00406; IgV; 1.			
DR	PROSITE; PS00835; IG-LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; 1.			
KW	Hypothetical protein.			
SK	SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;			

Query Match	88.8%	Score 1103;	DB 4;	Length 239;
Best Local Similarity	88.7%	Pred. No. 3.6e-93;		
Matches 212;	Conservative 15;	Mismatches 12;	Indels 0;	Gaps 0;
QY	1	MSLPAQLGLLLCVPGSSGEVMTQSPSLPITPGEFASISCRSSQSLKHSNGDTFLSW	60	
Db	1	MSLPAQLGLLLCVPGSSGDVMTQSPSLPVLTPGASISCRSTQSLVSDGNTYLNW	60	
QY	61	YQKFGQSPRLIIYKVNSRDSVPRFSGSGAGTFTLKISAVEAEDGVVFCGGGTTP	120	
Db	61	FQCRFGQSPRLIIYKVNSRDSVPRFSGSGAGTFTLKIRVEAEDGVVFCMGGTWP	120	

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QY 121 PTFGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVGVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 STFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVGVCLLNNFYPREAKVQWKVDNALQ 180
QY 181 SGNQSQSVTEQDSKDYSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSQSVTEQDSKDYSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 2
Q8NEK0
ID Q8NEK0 PRELIMINARY; PRT; 239 AA.
AC Q8NEK0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 87.4%; Score 1086; DB 4; Length 239;
Best Local Similarity 87.9%; Pred. No. 1.3e-91;
Matches 210; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLPAQLLGLLLCPGSSGEVVMQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSW 60
Db 1 MRLPAQLLGLLLMWVSGSGDIYMTQSPATLSVSPGERATLSCRASQSVT-SN----LAW 55
QY 61 YQKPGQPPRLIYKVNRSNDSGVPDRFSGSGAGTDFTLKISAVEAEADVGVFCGQGRTP 120
Db 61 YLQKPGSQQLLIYLGNSRASGVDPDRFSGSGAGTDFTLKISAVEAEADVGVFCGQGRTP 120
QY 121 PTFGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVGVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 QTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVGVCLLNNFYPREAKVQWKVDNTLQ 180
QY 181 SGNQSQSVTEQDSKDYSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSQSVTEQDSKDYSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3
Q8NEK1
ID Q8NEK1 PRELIMINARY; PRT; 234 AA.
AC Q8NEK1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030813; AAH30813.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 6316B8DEF8D132F8 CRC64;

Query Match 76.4%; Score 949.5; DB 4; Length 234;
Best Local Similarity 77.8%; Pred. No. 4.3e-79;
Matches 186; Conservative 24; Mismatches 24; Indels 5; Gaps 2;

QY 1 MSLPAQLLGLLLCPGSSGEVVMQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSW 60
Db 1 MEAPAQLLFLLLLWLPDPTTGIVMTQSPATLSVSPGERATLSCRASQSVT-SN----LAW 55
QY 61 YQKPGQPPRLIYKVNRSNDSGVPDRFSGSGAGTDFTLKISAVEAEADVGVFCGQGRTP 120
Db 56 YQQTFGQSPRLVIYGASSRASGVDPDRFSGSGAGTDFTLTISLQSEDFAVVYCOQYNKWP 115
QY 121 PTFGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVGVCLLNNFYPREAKVQWKVDNALQ 180
Db 116 HTFGQGTKLDIKRTVAAPSVFIFPPSDEQLKSGTASVGVCLLNNFYPREAKVQWKVDNALQ 175
QY 181 SGNQSQSVTEQDSKDYSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 176 SGNQSQSVTEQDSKDYSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 4
Q8VCi6
ID Q8VCi6 PRELIMINARY; PRT; 238 AA.
AC Q8VCi6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 69.6%; Score 864.5; DB 11; Length 238;
Best Local Similarity 68.2%; Pred. No. 2.8e-71;
Matches 163; Conservative 30; Mismatches 45; Indels 1; Gaps 1;

QY 1 MSLPAQLLGLLLCPGSSGEVVMQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVRL--VLMFWIPASSDVVMVTPSLPVSIGDQASISCRSSQSLVHSNGNTVLHW 59
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:12:09 ; Search time 10.6148 Seconds

(without alignments)
952.662 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSLPAQLGLLLCVPGSSG.....EVTHQGLSPVTKSNRGRPC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	239	3	US-08-487-550-6
2	1242	100.0	239	4	US-09-526-098-6
3	978	78.7	241	2	US-07-916-098A-56
4	976	78.6	242	1	US-08-398-613A-56
5	976	78.6	242	1	US-08-398-612A-56
6	976	78.6	242	1	US-08-398-611A-56
7	976	78.6	242	2	US-08-491-334A-56
8	976	78.6	242	3	US-09-027-449-42
9	976	78.6	242	3	US-08-804-444A-42
10	976	78.6	242	3	US-09-026-985-42
11	976	78.6	242	4	US-09-121-952A-42
12	976	78.6	242	4	US-09-234-340A-42
13	975.5	78.5	240	4	US-09-301-593-36
14	939.5	75.6	234	3	US-09-049-672A-6
15	936	75.4	242	3	US-09-027-449-62
16	936	75.4	242	3	US-09-026-985-62
17	936	75.4	242	4	US-09-121-952A-62
18	936	75.4	242	4	US-09-234-340A-62
19	935	75.3	242	3	US-09-027-449-51
20	935	75.3	242	3	US-08-804-444A-51
21	935	75.3	242	3	US-09-026-985-51
22	935	75.3	242	4	US-09-121-952A-51
23	935	75.3	242	4	US-09-234-340A-51
24	932	75.0	219	3	US-09-027-449-72
25	932	75.0	219	3	US-09-026-985-72
26	932	75.0	219	4	US-09-121-952A-72
27	932	75.0	219	4	US-09-234-340A-72

28 932 75.0 242 3 US-09-027-449-56 Sequence 56, Appl
29 932 75.0 242 3 US-08-804-444A-56 Sequence 56, Appl
30 932 75.0 242 3 US-09-026-985-56 Sequence 56, Appl
31 932 75.0 242 4 US-09-121-952A-56 Sequence 56, Appl
32 932 75.0 242 4 US-09-234-340A-56 Sequence 56, Appl
33 928.5 74.8 240 4 US-09-301-593-28 Sequence 28, Appl
34 909.5 73.2 220 3 US-08-952-235-1 Sequence 1, Appl
35 909.5 73.2 220 4 US-09-669-971-1 Sequence 1, Appl
36 904.5 72.8 234 4 US-09-740-002-24 Sequence 24, Appl
37 900.5 72.5 235 3 US-08-812-586-16 Sequence 16, Appl
38 900.5 72.5 235 4 US-09-535-832A-17 Sequence 17, Appl
39 900 72.5 235 1 US-08-276-852-153 Sequence 153, App
40 900 72.5 235 1 US-08-899-575-153 Sequence 153, App
41 900 72.5 235 1 US-08-899-575-153 Sequence 153, App
42 900 72.5 235 5 PCT-US95-08743-153 Sequence 153, App
43 899.5 72.4 236 1 US-08-157-101A-5 Sequence 5, Appl
44 893.5 71.9 218 5 PCT-US96-13152-2 Sequence 2, Appl
45 893.5 71.9 220 4 US-09-301-593-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-6
; Sequence 6, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-6

Query Match 100.0%; Score 1242; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.9e-101;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSSGGEVVMPTQSLPITTFGEPAISICRSSQSLKHSNGDTFLSW 60
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DB 1 MSLPAQLGLLLCVPGSSGGEVVMPTQSLPITTFGEPAISICRSSQSLKHSNGDTFLSW 60
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QY 61 YQKPGQPPRLIIYKYSNRDSDGVPDRFSGSGAGTDTTLKISAVEAEDVGVYFCGGGTRTP 120
 Db 61 YQKPGQPPRLIIYKYSNRDSDGVPDRFSGSGAGTDTTLKISAVEAEDVGVYFCGGGTRTP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQ 180
 Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQ 180
 QY 181 SGNQSESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 181 SGNQSESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 2

US-09-526-098-6
 ; Sequence 6, Application US/09526098
 ; Patent No. 6492134
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Daiell R.
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 ; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/526,098
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/383,916
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/487,550
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-131
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 239 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-526-098-6

Query Match 100.0%; Score 1242; DB 4; Length 239;
 Best Local Similarity 100.0%; Pred. No. 3.9e-101;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSGEVVMTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
 Db 1 MSLPAQLGLLLLCVPGSGEVVMTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
 QY 61 YQKPGQPPRLIIYKYSNRDSDGVPDRFSGSGAGTDTTLKISAVEAEDVGVYFCGGGTRTP 120
 Db 61 YQKPGQPPRLIIYKYSNRDSDGVPDRFSGSGAGTDTTLKISAVEAEDVGVYFCGGGTRTP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQ 180

Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQ 180
 QY 181 SGNQSESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 181 SGNQSESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3

US-07-916-098A-56
 ; Sequence 56, Application US/07916098A
 ; Patent No. 5871732
 ; GENERAL INFORMATION:
 ; APPLICANT: BURKLY, LINDA C.
 ; APPLICANT: CHISHOLM, PATRICIA L.
 ; APPLICANT: THOMAS, DAVID W.
 ; APPLICANT: ROSA, MARGARET D.
 ; APPLICANT: ROSA, JOSEPH J.
 ; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 ; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
 ; STREET: 10 SOUTH WACKER DRIVE
 ; CITY: CHICAGO
 ; STATE: ILLINOIS
 ; COUNTRY: U.S.A.
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/916.098A
 ; FILING DATE: July 24, 1992
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/08843
 ; FILING DATE: No. 5871732member 27, 1991
 ; CLASSIFICATION: 424
 ; APPLICATION NUMBER: 07/618,542
 ; FILING DATE: No. 5871732member 27, 1990
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: JOHN J. MC DONNELL
 ; REGISTRATION NUMBER: 26,949
 ; REFERENCE/DOCKET NUMBER: 92,310-G
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 715-1000
 ; TELEFAX: (312) 715-1234
 ; TELEX: 910/221-5317
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 241 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-916-098A-56

Query Match 78.7%; Score 978; DB 2; Length 241;
 Best Local Similarity 80.4%; Pred. No. 4.7e-78;
 Matches 193; Conservative 22; Mismatches 23; Indels 2; Gaps 2;

QY 1 MSLPAQLGLLLLCVPGSGEVVMTQSPSLPTTPGEPASISCRSSQSLKHS-NGDTFLS 59
 Db 3 MRVPAQLGLLLWLPGARGDIVMTQSPDSLAVSLGERATINCKSSGLLSTQKNYLA 62
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 Db 63 WYQKPGQPPRLIIYKYSNRDSDGVPDRFSGSGAGTDTTLTSSLAEDVAVYIC-QQYYS 121
 QY 120 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNAL 179

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:18:44 ; Search time 89.7228 Seconds
(without alignments)
421.442 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSIPAGLLGLLLCPGSSG.....EVTHQGLSPYTKSFNRGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1242	100.0	239	12	US-10-291-532-6
4	1242	100.0	239	14	US-10-124-905-6
5	1068	86.0	239	11	US-09-992-600A-8
6	1068	86.0	239	11	US-09-924-340-8
7	1068	86.0	239	12	US-09-992-095B-8
8	1068	86.0	239	12	US-10-154-678-8
9	1068	86.0	239	12	US-09-999-570-8
10	1068	86.0	239	15	US-10-000-489-8
11	1068	86.0	239	15	US-10-000-986-8
12	1008	81.2	219	11	US-09-972-656-92
13	1003.5	80.8	238	15	US-10-171-452A-38
14	1003.5	80.8	238	15	US-10-171-452A-56
15	997	80.3	219	11	US-09-972-656-106

16	993.5	80.0	238	15	US-10-171-452A-44
17	993.5	80.0	238	15	US-10-171-452A-50
18	992.5	79.9	220	10	US-09-822-698A-24
19	991	79.8	219	11	US-09-972-656-104
20	977	78.7	219	11	US-09-972-656-94
21	976.5	78.6	238	12	US-10-384-933-107
22	976.5	78.6	238	15	US-10-216-484-107
23	976	78.6	242	11	US-09-726-258-42
24	975.5	78.5	240	12	US-10-159-006-36
25	971.5	78.2	238	12	US-10-384-933-109
26	971.5	78.2	238	12	US-10-216-484-109
27	970.5	78.1	238	12	US-10-384-933-54
28	970.5	78.1	238	15	US-10-216-484-54
29	969	78.0	235	15	US-10-153-382-7
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31	965.5	77.7	238	15	US-10-216-484-52
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34	963	77.5	233	15	US-10-153-382-11
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36	960	77.3	239	10	US-09-249-011A-22
37	958.5	77.2	218	15	US-10-171-452A-39
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39	957.5	77.1	234	15	US-10-153-382-15
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41	955.5	76.9	234	12	US-09-848-832-4
42	954.5	76.9	240	9	US-09-799-514-8
43	948.5	76.4	218	15	US-10-171-452A-45
44	948.5	76.4	218	15	US-10-171-452A-51
45	948.5	76.4	238	12	US-10-384-933-129

ALIGNMENTS

RESULT 1

US-09-948-429B-6
; Sequence 6, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/948.429B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELEPHONE/INFORMATION:

TELEPHONE: 703-836-6620


```
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-6

Query Match          100.0%; Score 1242; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLLGLLLCVPGSSGEVVMQSPLSLPIITGPEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLLGLLLCVPGSSGEVVMQSPLSLPIITGPEPASISCRSSQSLKHSNGDTFLSW 60
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DB 61 YQKPGQPRLIIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGGTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
QY 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
DB 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 2
US-10-124-807-6
; Sequence 6, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-807-6

Query Match          100.0%; Score 1242; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLPAQLLGLLLCVPGSSGEVVMQSPLSLPIITGPEPASISCRSSQSLKHSNGDTFLSW 60
QY 61 YQKPGQPRLIIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGGTRTP 120
DB 61 YQKPGQPRLIIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGGTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
QY 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
DB 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3
US-10-291-532-6
; Sequence 6, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/383,916
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 08/487,950
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primatized peptide sequence
US-10-291-532-6

Query Match          100.0%; Score 1242; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLLGLLLCVPGSSGEVVMQSPLSLPIITGPEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLLGLLLCVPGSSGEVVMQSPLSLPIITGPEPASISCRSSQSLKHSNGDTFLSW 60
QY 61 YQKPGQPRLIIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGGTRTP 120
DB 61 YQKPGQPRLIIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGGTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:01:50 : Search time 3774.61 Seconds
(without alignments)
15574.362 Million cell updates/sec

Title: US-09-758-173-7
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Sequence: 1 ATGGGTGGAGCCTCATCTT.....CCCTGTCGCCGGTAAATGA 1437

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 8: gb_pl.*
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- 10: gb_ro.*
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- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
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- 33: em_hgt_mus.*
- 34: em_hgt_pln.*
- 35: em_hgt_rod.*
- 36: em_hgt_mam.*
- 37: em_hgt_vrt.*
- 38: em_sy.*
- 39: em_hgtgo_hum.*
- 40: em_hgtgo_mus.*
- 41: em_hgtgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1437	100.0	1437	6	AR108865	Sequence AR108865
2	1437	100.0	1437	6	AR265199	Sequence AR265199
3	1437	100.0	1437	6	BD063037	Sequence BD063037
4	1238.6	86.2	1642	9	AK093806	Sequence AK093806
5	1219	84.8	1642	9	AK093806	Sequence AK093806
6	1208	84.1	1659	9	BC014667	Sequence BC014667
7	1189.2	82.8	1666	9	BC006402	Sequence BC006402
8	1188.2	82.7	1679	9	BC018747	Sequence BC018747
9	1186.2	82.5	1630	9	BC024289	Sequence BC024289
10	1185	82.5	1425	9	AY172959	Sequence AY172959
11	1185	82.5	1430	9	AX419496	Sequence AX419496
12	1184.6	82.4	1549	6	A21385	Sequence A21385
13	1184	82.4	1673	9	HSIGSLH	Sequence HSIGSLH
14	1183.4	82.4	1633	9	AK097859	Sequence AK097859
15	1183	82.3	1630	9	BC041037	Sequence BC041037
16	1182.2	82.3	1990	9	AK098817	Sequence AK098817
17	1177.8	82.0	19040	6	BD075127	Sequence BD075127
18	1173	81.6	1631	9	AK097010	Sequence AK097010
19	1171.8	81.5	3143	9	BC019046	Sequence BC019046
20	1169.4	81.4	1624	9	HSIGSLH	Sequence HSIGSLH
21	1166.6	81.2	1633	9	AK097367	Sequence AK097367
22	1162.2	80.9	1419	12	AF019036	Sequence AF019036
23	1157.4	80.5	1404	9	AF027159	Sequence AF027159
24	1155	80.4	1627	9	AK097350	Sequence AK097350
25	1155	80.4	1639	9	AK097950	Sequence AK097950
26	1148.2	79.9	1624	9	AK097206	Sequence AK097206
27	1147.8	79.9	1392	6	AX594307	Sequence AX594307
28	1147.8	79.9	1392	6	AX616608	Sequence AX616608
29	1147.8	79.9	1392	6	AX616908	Sequence AX616908
30	1147.8	79.9	9568	6	AX616611	Sequence AX616611
31	1147.2	79.8	1335	6	AX010615	Sequence AX010615
32	1147.2	79.8	1335	6	AX010646	Sequence AX010646
33	1141.4	79.4	1431	9	AY172957	Sequence AY172957
34	1141.4	79.4	1620	9	AK097366	Sequence AK097366
35	1140	79.3	1353	6	AX277242	Sequence AX277242
36	1139.8	79.3	1618	9	AK097360	Sequence AK097360
37	1138.6	79.2	1637	9	AK093636	Sequence AK093636
38	1133.4	78.9	1599	6	AX330501	Sequence AX330501
39	1133.4	78.9	1599	6	AX333307	Sequence AX333307
40	1133.4	78.9	1599	6	AX334122	Sequence AX334122
41	1133.4	78.9	1599	9	HUMISHEPAH	Sequence HUMISHEPAH
42	1131.8	78.8	1617	6	A29585	Sequence A29585
43	1130.2	78.6	1449	6	BD078407	Sequence BD078407
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ALIGNMENTS

RESULT 1	AR108865	Sequence 7 from patent US 6113898.	1437 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR108865	Sequence 7 from patent US 6113898.				
DEFINITION	AR108865					
ACCESSION	AR108865					
VERSION	AR108865.1	GI:12825141				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1437)					
AUTHORS	Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.					
TITLE	Human B7.1-specific primatized antibodies and transfectomas					
JOURNAL	expressing said antibodies					
	Patent: US 6113898-A 7 05-SEP-2000;					

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	Best Local Similarity	100.0%; Pred. No. 1.3e-280;		
	Matches 1437; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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QY	61	GTCACACTGGTGGAGTCTGGGGAGGCTTGTCCAGCCTGGCGGTCCCTGAGAGTCTCC	120	
DB	61	GTCACACTGGTGGAGTCTGGGGAGGCTTGTCCAGCCTGGCGGTCCCTGAGAGTCTCC	120	
QY	121	TGTGCAGTCTCTGGATTCACTTCAGTGACCACCTACATGTATTGGTTCCGCCAGGCTCCA	180	
DB	121	TGTGCAGTCTCTGGATTCACTTCAGTGACCACCTACATGTATTGGTTCCGCCAGGCTCCA	180	
QY	181	GGGAAGGGCGGGAATGGTAGTTTCATTAAGAACAACACCGAACCGGTGGGCAACAGAA	240	
DB	181	GGGAAGGGCGGGAATGGTAGTTTCATTAAGAACAACACCGAACCGGTGGGCAACAGAA	240	
QY	241	TAGCCCGCTCTGTGAACACAGATTCCACTCTCCAGAGATGATTCCAAAGCATGCC	300	
DB	241	TAGCCCGCTCTGTGAACACAGATTCCACTCTCCAGAGATGATTCCAAAGCATGCC	300	
QY	301	TATCTCAAAATGAGCAGCCTGAAAATCAGGAGCACGGCCGTCTATTACTGTACTACATCC	360	
DB	301	TATCTCAAAATGAGCAGCCTGAAAATCAGGAGCACGGCCGTCTATTACTGTACTACATCC	360	
QY	361	TACATTTACATGTGCGGTGGTCTGCTATGAGGTACTTCGAATTCGGGGCCAG	420	
DB	361	TACATTTACATGTGCGGTGGTCTGCTATGAGGTACTTCGAATTCGGGGCCAG	420	
QY	421	GGCGCCCTGGTCAACGCTCTCCAGTACGACCAAGAGGCCCATGGCTTCCCCTGGCA	480	
DB	421	GGCGCCCTGGTCAACGCTCTCCAGTACGACCAAGAGGCCCATGGCTTCCCCTGGCA	480	
QY	481	CCCTCTCTCAAGAGCACCTCTGGGGGCACAGGGCCCTGGGCTGGTTCAGGATAC	540	
DB	481	CCCTCTCTCAAGAGCACCTCTGGGGGCACAGGGCCCTGGGCTGGTTCAGGATAC	540	
QY	541	TTCCCCGAACCGGTGACGGTCTGCTGGAACCTCAGCGCCCTGACAGCGGGTGCACACC	600	
DB	541	TTCCCCGAACCGGTGACGGTCTGCTGGAACCTCAGCGCCCTGACAGCGGGTGCACACC	600	
QY	601	TTCCCGGCTGCTCAGACTCTCAGGACTCTACTCCCTCAGCAGGGTGGTACCGTCCCC	660	
DB	601	TTCCCGGCTGCTCAGACTCTCAGGACTCTACTCCCTCAGCAGGGTGGTACCGTCCCC	660	
QY	661	TCACAGCAGTCTGGGACCCAGACCTTACATCTGCAAGTGAATCAAGCCCGCAACACC	720	
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QY	781	CAGACACCTTGAATCTCTGGGGGACCGTCACTCTCTCTTCCCTCCCGCCCAACAGGAC	840	
DB	781	CAGACACCTTGAATCTCTGGGGGACCGTCACTCTCTCTTCCCTCCCGCCCAACAGGAC	840	
QY	841	ACCTCATGATCTCCCGGACCCCTGAGTGCATCTGCTGTGGTGGTGGAGCTGAGCCAGAA	900	
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DB	1261	AATAAGACACACCCCTCCCGTGTGACTCCGACGCTCTCTTCTTCTCTACAGCAAG	1320	
QY	1321	CTCACCGTGGACAAGCAGGTGGCAGCAGGGAGACGCTCTCTCATGCTCGGTGATGCAT	1380	
DB	1321	CTCACCGTGGACAAGCAGGTGGCAGCAGGGAGACGCTCTCTCATGCTCGGTGATGCAT	1380	
QY	1381	GAGGCTCTGCAACACCACTACACGAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1437	
DB	1381	GAGGCTCTGCAACACCACTACACGAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1437	
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	DEFINITION	Accession AR265199		
	VERSION	AR265199.1	GT:29693620	
	KEYWORDS	Unknown.		
	SOURCE	Unknown.		
	ORGANISM	Unclassified.		
	REFERENCE	1 (bases 1 to 1437)		
	AUTHORS	Aquin,S. and Vezina,Louis,"P.		
	TITLE	Method for producing polyhydroxyalkanoates in recombinant organisms		
	JOURNAL	Patent: US 6492134-A 7 10-DEC-2002;		
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	Best Local Similarity	100.0%; Pred. No. 1.3e		

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 12:12:30 : Search time 294.323 seconds
(without alignments)
13179.730 Million cell updates/sec

Title: US-09-758-173-7
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
- 25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1437	100.0	1437	19 AAV35487	Macaque primatized
2	1437	100.0	1437	22 AAS17245	DNA sequence of a
3	1435.4	99.9	1437	18 AAT13847	Primate anti-hu
4	1219	84.8	7521	22 AAF30315	Bicistronic chimera
5	1216	84.6	1616	24 AAS62785	CDNA sequence #572
6	1199.2	83.5	1386	1 AQA9834	Anti-HIV-1 recombi
7	1186	82.5	1798	21 AAC98220	Human colon cancer
8	1185	82.5	1430	24 AAK98701	CDNA of the heavy

9	1185	82.5	1430	25	ABX12855	Human monoclonal I
10	1184	82.4	1644	22	AAS22593	Human cDNA encodin
11	1183	82.3	1549	13	AAQ20066	Encodes heavy chain
12	1182.2	82.3	19035	15	AAV61794	Traget plasmid Man
13	1178	82.0	1404	25	ABZ24633	Humanised 3b6 anti
14	1171.4	81.5	1427	19	AAV41431	Plasmid Hu19Hcped
15	1171.4	81.5	1427	19	AAV41432	Plasmid Hu19Hcped
16	1169.8	81.4	1427	19	AAV41429	Plasmid Hu19Hcped
17	1169.4	81.4	1442	22	AAC84208	Plasmid Glambda-1B
18	1166.2	81.2	6281	22	AAC84206	Plasmid Glambda-1A
19	1165.4	81.1	1615	24	ABK34973	Human cDNA encodin
20	1163	80.9	1617	24	AAS62784	cDNA sequence #571
21	1158.4	80.6	6284	19	AAV41427	Plasmid Hu19Hcped
22	1155.8	80.4	1576	14	AAQ45944	Human anti-HBs hea
23	1155.4	80.4	1641	15	AAQ54655	Human anti-HBs hea
24	1153.4	80.3	2974	22	AAH98397	Synthetic EST-deri
25	1147.8	79.9	1392	25	AAD53212	BIWA4 antibody DNA
26	1147.8	79.9	9568	25	AAD53219	Humanised anti-CD2
27	1147.2	79.8	1335	21	AAZ34748	Human cDNA encodin
28	1142.8	79.5	1598	24	ABK34965	cDNA sequence #303
29	1142.8	79.5	1634	24	AAS62515	Human recombinant
30	1141.4	79.4	1356	22	AAD20745	Mucin 1 (MUC-1) b1
31	1139.4	79.3	1412	13	AAQ25692	Sequence of the ch
32	1138.6	79.2	1347	21	AAZ60599	cDNA encoding a ra
33	1138.6	79.2	1590	24	ABK34976	Human cDNA encodin
34	1138.6	79.2	1640	24	ABK35183	Human cDNA encodin
35	1133.4	78.9	1599	24	ABK64550	Human benign prost
36	1133.4	78.9	1599	24	ABL62673	Colon adenocarcino
37	1133.4	78.9	1599	24	ABL65479	Lung cancer relate
38	1133.4	78.9	1599	24	ABL66294	Lung cancer relate
39	1131.8	78.8	1617	14	AAQ35099	Antibody D heavy c
40	1130.2	78.6	1449	20	AAQ06951	Monoclonal antibod
C 42	1130.2	78.6	1449	20	AAQ06952	Monoclonal antibod
C 43	1129.2	78.6	9182	24	ABK10574	Baculovirus expres
C 44	1127.8	78.5	1467	13	AAQ23570	Reshaped CAMPARF-1
C 45	1127.6	78.5	9182	24	ABL55051	Plasmid pTRABac/9F

ALIGNMENTS

RESULT 1

AAV35487	AAV35487 standard; DNA; 1437 BP.
ID	AAV35487
XX	AC
XX	AAV35487;
XX	29-SEP-1998 (first entry)
XX	Macaque primatized 7B6 heavy chain DNA.
DE	Monoclonal antibody; Mab; macaque; heavy chain; antigen; CD80;
KW	CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW	T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW	immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW	T cell proliferation; ss.
OS	Macaque fascicularis.
XX	Key
XX	Location/Qualifiers
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FT	/tag= a
FT	/product= 7B6 heavy chain
XX	WO9819706-A1.
PN	14-MAY-1998.
XX	29-OCT-1997;
XX	97MO-US19906.
XX	08-NOV-1996;
XX	96US-0746361.

PA (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Brams P, Hanna N;
 XX WPI; 1998-286601/25.
 DR P-PSDB; AAW63763.
 XX
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 XX Example 7; Fig 4b; 87pp; English.
 XX
 CC This sequence encodes a primatized form of the antibody 7B6 heavy chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 XX Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;
 SQ
 Query Match 100.0%; Score 1437; DB 19; Length 1437;
 Best Local Similarity 100.0%; Pred. No. 1.1e-277;
 Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 GTCAACTGTGTGAGTCTGGGGAGGCTTGTGTCAGCCGTCGCGGTGTCAGTGTGTC 120
 DB 61 GTCAACTGTGTGAGTCTGGGGAGGCTTGTGTCAGCCGTCGCGGTGTCAGTGTGTC 120
 QY 121 TGTGCACTCTCTGGAATTCACCTTCAGTGACCACTACATGATATGTTGTCGCGAGGCTCCA 180
 DB 121 TGTGCACTCTCTGGAATTCACCTTCAGTGACCACTACATGATATGTTGTCGCGAGGCTCCA 180
 QY 181 GGAAGGGGCGGAATGGGTAGTGTTCATTAGAAACAAACCGAAGCGTGGGACACAGAA 240
 DB 181 GGAAGGGGCGGAATGGGTAGTGTTCATTAGAAACAAACCGAAGCGTGGGACACAGAA 240
 QY 241 TAGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCGCAAGATCGCC 300
 DB 241 TAGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCGCAAGATCGCC 300
 QY 301 TATCTCAATGAGCAGCTGAAATTCGAGGACAGCGCGCTATATCTGTTACTATCATCC 360
 DB 301 TATCTCAATGAGCAGCTGAAATTCGAGGACAGCGCGCTATATCTGTTACTATCATCC 360
 QY 361 TACATTTACATGTCGGGTGGTGTCTGCTATGAGGATTTACTTGAATTCCTGGGCGCAG 420
 DB 361 TACATTTACATGTCGGGTGGTGTCTGCTATGAGGATTTACTTGAATTCCTGGGCGCAG 420
 QY 421 GGGCGGCTGGTACCGTCTCTCAGTACACCAAGGCGCCATCGTCTCCCGCTGGCA 480
 DB 421 GGGCGGCTGGTACCGTCTCTCAGTACACCAAGGCGCCATCGTCTCCCGCTGGCA 480
 QY 481 CCCTCTCCAAAGACACCTCTGGGGGCACAGCGGCGCTGGCTGGCTGAAGACTAC 540
 DB 481 CCCTCTCCAAAGACACCTCTGGGGGCACAGCGGCGCTGGCTGGCTGAAGACTAC 540

DB 481 CCCTCTCCAAAGACACCTCTGGGGGCACAGCGGCGCTGGCTGGCTGAAGACTAC 540
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 DB 541 TTCCCGGAACCGGTGACGGTGTGCTGGAACACTCAGCGGCCCTGACACAGCGGCTGACACACC 600
 QY 601 TTCCCGGGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGGCTGTCACCGTGCCTGCC 660
 DB 601 TTCCCGGGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGGCTGTCACCGTGCCTGCC 660
 QY 661 TCCAGCAGCTTGGGCACCCAGACCTACATCTCTCAACGTGAATCAAGCCCAAGCAACACC 720
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 DB 721 AAGTGTGACAAAGACAGCCCAAACTTGTGCAAACTCACAATGCCACCGTGC 780
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 DB 781 CCAGCAGCTGAACCTCTCTGGGGGACCGTCACTCTCTCTTCCCGCCCAAAACCCCAAGGAC 840
 QY 841 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCAGCA 900
 DB 841 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCAGCA 900
 QY 901 GACCTGAGGTCAAGTTCAACTGGTACGTGGACGCGCTGGAGGTGCATATGCCAAGACA 960
 DB 901 GACCTGAGGTCAAGTTCAACTGGTACGTGGACGCGCTGGAGGTGCATATGCCAAGACA 960
 QY 961 AAGCGCGGGAGGAGCAGTACAACAGCAGTACCTGTGTGTCAGCTGCTCACCCTGCTG 1020
 DB 961 AAGCGCGGGAGGAGCAGTACAACAGCAGTACCTGTGTGTCAGCTGCTCACCCTGCTG 1020
 QY 1021 CACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGTCTCCAAAGACCCCTCCCA 1080
 DB 1021 CACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGTCTCCAAAGACCCCTCCCA 1080
 QY 1081 GCCCGCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAGCAATGGCAGGAGTAC 1140
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 DB 1141 ACCCTGCCCATCCCGGATGAGTGACCAAGAACAGGTCAGCTGACCTGCTGCTGCTGTC 1200
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 DB 1201 AAAGCTTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGCAGCGGAGAAC 1260
 QY 1261 AACTACAGACACCGCTCCCGTGTGACTCCGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
 DB 1261 AACTACAGACACCGCTCCCGTGTGACTCCGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
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 DB 1321 CTCACCGTGGACAGAGAGTGGCAGCGGGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
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 DB 1381 GAGCTCTGCACACCACTACACGCAAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1437

RESULT 2
 AASI7245
 ID AASI7245 standard; DNA; 1437 BP.
 XX
 AC AASI7245;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE DNA sequence of a primatised form of the heavy chain of 7B6 antibody.
 XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 13:05:20 ; Search time 2376.47 Seconds
(without alignments)
14696.420 Million cell updates/sec

Title: US-09-758-173-7
Perfect score: 1437
Sequence: 1 ATGGGTGGAGCTCATCT.....CCCTGCTCCGGGTAATGA 1437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
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8: em_estt.*
9: gb_est1.*
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28: gb_gss1.*
29: gb_gss2.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	948.2	66.0	1201	13	BX377695
c 2	929.6	64.7	1142	13	BX414495
c 3	902	62.8	1020	12	BQ062878
c 4	899.2	62.6	1045	13	BX337477

c 5	894.8	62.3	1149	13	BX381020
c 6	892.6	62.1	1201	13	BX377803
c 7	891.2	62.0	1201	13	BX439438
c 8	889.8	61.9	902	13	BX439438
c 9	885.8	60.9	1013	13	BX360518
c 10	867.6	60.4	1200	13	BX415883
c 11	864	60.1	947	13	BQ709771
c 12	850.4	59.2	958	13	BQ706140
c 13	849.2	59.1	1093	13	BX428863
c 14	842.4	58.6	926	10	BG755166
c 15	837.4	58.3	988	13	BQ708857
c 16	832	57.9	1096	13	BX415920
c 17	831.8	57.9	1201	13	BX338493
c 18	830.8	57.8	901	12	BM007892
c 19	830.6	57.8	985	13	BX457369
c 20	829.4	57.7	1201	13	BX417147
c 21	824.4	57.4	1029	12	BQ063185
c 22	823.8	57.3	918	13	BQ708022
c 23	823.2	57.3	1019	13	BX325650
c 24	822.8	57.3	887	13	BQ711255
c 25	819	57.0	995	12	BM914540
c 26	818	56.9	1015	13	BX367600
c 27	817.8	56.9	980	13	BX325701
c 28	811.8	56.5	889	13	BX345909
c 29	811	56.4	1147	13	BX360330
c 30	809	56.3	1009	13	BX456658
c 31	808.8	56.3	881	13	BQ711291
c 32	807.4	56.2	1200	13	BX456326
c 33	804	55.9	853	13	BX388631
c 34	801.6	55.8	862	13	BX450248
c 35	800.2	55.7	1031	13	BQ064886
c 36	799.4	55.6	852	13	BX450232
c 37	798.4	55.6	1004	13	BX432300
c 38	797.4	55.5	936	13	BQ71127
c 39	796	55.4	940	13	BQ705928
c 40	795.6	55.4	1070	13	BX397632
c 41	795.2	55.3	1152	13	BX339318
c 42	794.2	55.3	1151	13	BX378450
c 43	792.2	55.1	885	13	BX408117
c 44	791.2	55.1	1201	13	BX396322
c 45	788.8	54.9	1201	13	BX439176

ALIGNMENTS

RESULT 1
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LOCUS 1201 bp mRNA linear EST 08-MAY-2003
DEFINITION BX377695 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI009YJ10 3-PRIME, mRNA sequence.

ACCESSION BX377695

VERSION BX377695.1

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

UNPUBLISHED

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7198.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI009DE05NP1cluster=7198.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI009DE05NP1.

FEATURES

source

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
BASE COUNT	188 a 296 c 396 g 267 t 54 others
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QY	521 GTCGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTCGTGAACCTCAGCGGCC 580
DB	1003 GCTGCCTCTGTCAAGGACTACTTCCCGAACCG-GTGACGGTGTCTCGTGAACCTCAGCGGCC 945
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DB	645 TGTGTGACGTGACCGACGACGACCTGATCTCAAGTTCAACTGGTACGTGGAGCGGTGG 586
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10

D	B		346	TCAGCGTACCTGCCTGGTCAAAGGCTTTATCCAGCAGCATCGCGTGAGTGGAGA	287
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D	B		226	CCTTCTTCCTCTACAGCAAGCTCACCGTGCAGACAGCAGGTGGCAGCGGAACGCTCT	167
Q	Y		1361	TCTCATGCTCCGGTAGCATGAGGCTCTGCACAAACCATTACAGCAGACAGAGCTCTCCC	1420
D	B		166	TCTCATGCTCCGGTAGCATGAGGCTCTGCACAAACCATTACAGCAGACAGAGCTCTCCC	107
Q	Y		1421	TGTCCTCCGGTAAATGA	1437
D	B		106	TTTCTCCGGTAAATGA	90

RESULT 2
BX414495/c
LOCUS
DEFINITION
3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1142)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSOCAP001AE07NP1&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP001AE07NP1.

FEATURES

Source

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1. .1142
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
193 a 290 c 381 g 27 others
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Best Local Similarity 98.2%; Pred. No. 3.6e-205;
Matches 952; Conservative 6; Mismatches 9; Indels 2; Gaps 2;

```

469 TTCCCTCGGCACCTCCTCCAAAGCACACCCTCTGGGGGACACAGGGGCCCTGGGTGCCTG 528
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1078 TTTCCCTTGACCTCCTCAAAGAGMACTTCTGGGG-ANAGSGCCCTGGGCTGCCTG 1020

529 GTCAGGACTACTTCCCAGAACCGGTGACGGTGTGCTGGAACTCAAGGGCCCTGACCAAGC 588